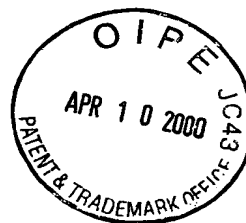


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SEQUENCE LISTING

<110> Abbott Laboratories  
Schlauder, George G.  
Erker, James C.  
Desai, Suresh M.  
Dawson, George J.  
Mushahwar, I. K.

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 <223> us1-733wb  
  
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 <223> us1 733s1  
  
 <400> 61  
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<212> DNA
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<223> us2851-r2

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<212> DNA
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<223> us1 733s2

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 <223> us2-579-s1  
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 <212> DNA  
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 <223> JE hev167-a1  
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 <210> 71  
 <211> 22



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<212> DNA
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<223> us2-579-s2

<400> 71
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<210> 72
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<212> DNA
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<223> JE hev167-a2

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<223> us2-430s1

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<210> 85

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<210> 87
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 <213> Hepatitis E Virus

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 <223> us1full

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aa

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<210> 90
<211> 7202
<212> DNA
<213> Hepatitis E Virus

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<220>
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<222> (1)...(5094)
<223> Orf1

```

```

<221> CDS
<222> (5132)...(7111)
<223> Orf2

```

```

<223> Orf3 at positions 5094-5462

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<223> Xaa = Unknown or Other at position 174

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<223> Xaa = Unknown or Other at position 363

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<223> Xaa = Unknown or Other at position 1088

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<223> Xaa = Unknown or Other at position 1131

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<223> Xaa = Unknown or Other at position 1217

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<223> Xaa = Unknown or Other at position 1389

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<223> Xaa = Unknown or Other at position 2179

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<223> Xaa = Unknown or Other at position 2240

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<223> Xaa = Unknown or Other at position 2293

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<400> 90

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tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tct cgc gtg	96
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val	
20 25 30	
caa acc gag att ctt att aat ttg atg caa ccc cgg cag ttg gtt ttc	144
Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe	
35 40 45	
cgc cct gag gta ctt tgg aat cac cct atc cag cgg gtt ata cat aat	192
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn	
50 55 60	
gaa tta gaa cag tac tgc cgg gct cgg gct ggt cgt tgc ttg gag gtt	240
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val	
65 70 75 80	
gga gct cac cca aga tcc att aat gac aac ccc aac gtt ctg cat cgg	288
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg	
85 90 95	
tgt ttc ctt aga ccg gtt ggc cga gat gtt cag cgc tgg tac tct gcc	336
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc acc cgc ggc cct gcg gct aat tgc cgc cgc tcc gcg ttg cgt ggt	384
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctc ccc ccc gct gac cgc act tac tgc ttt gat gga ttc tcc cgt tgt	432
Leu Pro Pro Ala Asp Arg Thr Tyr Cys Phe Asp Gly Phe Ser Arg Cys	
130 135 140	
gct ttt gct gca gag acc ggt gtg gct ctt tac tct ctg cat gac ctt	480
Ala Phe Ala Ala Glu Thr Gly Val Ala Leu Tyr Ser Leu His Asp Leu	
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Trp Pro Ala Asp Val Ala Glu Ala Met Ala Arg His Gly Xaa Thr Arg	
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Leu Tyr Ala Ala Leu His Leu Pro Pro Glu Val Leu Leu Pro Pro Gly	
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Thr Tyr His Thr Thr Ser Tyr Leu Leu Ile His Asp Gly Asp Arg Ala	
195 200 205	
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Val Val Thr Tyr Glu Gly Asp Thr Ser Ala Gly Tyr Asn His Asp Val	
210 215 220	
tcc ata ctt cgt gcg tgg atc cgt act aca aaa ata gtt ggt gat cat	720



Ser 225	Ile	Leu	Arg	Ala	Trp 230	Ile	Arg	Thr	Thr	Lys 235	Ile	Val	Gly	Asp	His 240	
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Pro	Leu	Val	Ile	Glu	Arg	Val	Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu	
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ctg	ctc	acc	gca	gcc	cct	gag	ccg	tca	ccc	atg	cct	tat	gtt	cct	tac	816
Leu	Leu	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr	
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cct	cgt	tca	acg	gag	gtg	tat	gtc	cgg	tcc	ata	ttt	ggc	cct	ggc	ggc	864
Pro	Arg	Ser	Thr	Glu	Val	Tyr	Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly	
		275					280					285				
tcc	cca	tcc	ttg	ttt	ccg	tca	gcc	tgc	tct	act	aaa	tct	act	ttc	cat	912
Ser	Pro	Ser	Leu	Phe	Pro	Ser	Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His	
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gct	gtc	ccg	gtg	cat	atc	tgg	gat	cgg	ctc	atg	ctc	ttt	ggt	gcc	acc	960
Ala	Val	Pro	Val	His	Ile	Trp	Asp	Arg	Leu	Met	Leu	Phe	Gly	Ala	Thr	
305					310				315						320	
ctg	gac	gat	cag	gcg	ttt	tgc	tgt	tca	cgg	ctc	atg	act	tac	ctc	cgt	1008
Leu	Asp	Asp	Gln	Ala	Phe	Cys	Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg	
			325					330					335			
ggt	att	agt	tac	aag	gtc	act	gtc	ggc	gcg	ctt	gtc	gct	aat	gag	ggg	1056
Gly	Ile	Ser	Tyr	Lys	Val	Thr	Val	Gly	Ala	Leu	Val	Ala	Asn	Glu	Gly	
			340					345					350			
tgg	aac	gcc	tct	gaa	gac	gct	ctt	act	gca	rtg	atc	act	gca	gct	tat	1104
Trp	Asn	Ala	Ser	Glu	Asp	Ala	Leu	Thr	Ala	Xaa	Ile	Thr	Ala	Ala	Tyr	
	355						360					365				
ttg	act	att	tgc	cat	cag	cgt	tat	ctc	cgc	acc	cag	gcg	ata	tcc	aag	1152
Leu	Thr	Ile	Cys	His	Gln	Arg	Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys	
	370					375					380					
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Gly	Met	Arg	Arg	Leu	Gly	Val	Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg	
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ctc	tac	agt	tgg	cta	ttt	gag	aag	tct	ggc	cgt	gat	tat	atc	ccc	ggc	1248
Leu	Tyr	Ser	Trp	Leu	Phe	Glu	Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly	
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cgc	cag	ctt	cag	ttc	tat	gca	cag	tgc	cga	cgg	tgg	cta	tct	gca	ggc	1296
Arg	Gln	Leu	Gln	Phe	Tyr	Ala	Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly	
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ttc	cac	cta	gac	ccc	agg	gta	ctt	gtt	ttt	gat	gag	tca	gta	cca	tgc	1344
Phe	His	Leu	Asp	Pro	Arg	Val	Leu	Val	Phe	Asp	Glu	Ser	Val	Pro	Cys	
	435					440						445				
cgc	tgt	agg	acg	ttt	ttg	aag	aaa	gtt	gcg	ggt	aaa	ttc	tgc	tgt	ttt	1392
Arg	Cys	Arg	Thr	Phe	Leu	Lys	Lys	Val	Ala	Gly	Lys	Phe	Cys	Cys	Phe	

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Met Arg Trp Leu Gly Gln Glu Cys Thr Cys Phe Leu Glu Pro Ala Glu			
465	470	475	480
ggg tta gtc ggc gat cat ggc cat gac aac gag gcc tat gag ggt tct			1488
Gly Leu Val Gly Asp His Gly His Asp Asn Glu Ala Tyr Glu Gly Ser			
	485	490	495
gag gtc gac ccg gct gaa cct gca cat ctt gat gtt tct ggg act tac			1536
Glu Val Asp Pro Ala Glu Pro Ala His Leu Asp Val Ser Gly Thr Tyr			
	500	505	510
gcc gtc cac ggg cac cag ctt gag gcc ctc tat agg gca ctt aat gtc			1584
Ala Val His Gly His Gln Leu Glu Ala Leu Tyr Arg Ala Leu Asn Val			
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cca caa gat att gcc gct cga gct tcc cga cta acg gca act gtt gag			1632
Pro Gln Asp Ile Ala Ala Arg Ala Ser Arg Leu Thr Ala Thr Val Glu			
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Leu Val Ala Ser Pro Asp Arg Leu Glu Cys Arg Thr Val Leu Gly Asn			
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Lys Thr Phe Arg Thr Val Val Asp Gly Ala His Leu Glu Ala Asn			
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ggc cct gag cag tat gtc tta tca ttt gac gcc tcc cgt cag tct atg			1776
Gly Pro Glu Gln Tyr Val Leu Ser Phe Asp Ala Ser Arg Gln Ser Met			
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ggg gcc ggg tcg cat agc ctc act tat gag ctc acc cct gct ggt ttg			1824
Gly Ala Gly Ser His Ser Leu Thr Tyr Glu Leu Thr Pro Ala Gly Leu			
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cag gtt agg att tca tct aat ggt ctg gat tgc act gct aca ttc ccc			1872
Gln Val Arg Ile Ser Ser Asn Gly Leu Asp Cys Thr Ala Thr Phe Pro			
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ccc ggt gga gcc cct agc gct gcg ccc ggg gag gtg gca gcc ttt tgc			1920
Pro Gly Gly Ala Pro Ser Ala Ala Pro Gly Glu Val Ala Ala Phe Cys			
	625	630	635
agt gcc ctt tat aga tat aac agg ttc acc cag cgg cac tcg ctg act			1968
Ser Ala Leu Tyr Arg Tyr Asn Arg Phe Thr Gln Arg His Ser Leu Thr			
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ggc gga tta tgg tta cac cct gag ggg ttg ctg ggt att ttc ccc cct			2016
Gly Gly Leu Trp Leu His Pro Glu Gly Leu Leu Gly Ile Phe Pro Pro			
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ttc tcc cct ggg cat atc tgg gag tct gcg aac ccc ttt tgc ggg gag			2064
Phe Ser Pro Gly His Ile Trp Glu Ser Ala Asn Pro Phe Cys Gly Glu			
	675	680	685

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ccc cct gtg cat aag cca tca ata ccc ccg cct tcc cgt aac cgt cgt Pro Pro Val His Lys Pro Ser Ile Pro Pro Pro Ser Arg Asn Arg Arg 770 775 780	2352
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gcg ttt tac cca act gaa ttc atc atg cgt gag ggt ctt gca gca tac Ala Phe Tyr Pro Thr Glu Phe Ile Met Arg Glu Gly Leu Ala Ala Tyr 835 840 845	2544
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gtt gag cag aac ccg aag agg ctt gag gca gcg tac cgt gaa act tgt Val Glu Gln Asn Pro Lys Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys 865 870 875 880	2640
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Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg Ser Leu Phe Trp	
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Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu Leu Thr Asp Ile	
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Gly	Asp	Ala	Tyr	Glu	Glu	Ser	Val	Phe	Ala	Ala	Ala	Val	Ser	Gly	Ala	
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Trp	Ile	Leu	Gln	Ala	Pro	Lys	Glu	Ser	Leu	Lys	Gly	Phe	Trp	Lys	Lys	
1505				1510				1515				1520				
cat	tct	ggg	gag	cct	ggg	acc	ctt	ctt	tgg	aat	acc	gtc	tgg	aat	atg	4608
His	Ser	Gly	Glu	Pro	Gly	Thr	Leu	Leu	Trp	Asn	Thr	Val	Trp	Asn	Met	
1525				1530				1535								
gcg	att	ata	gca	cat	tgc	tat	gag	ttc	cgt	gac	ttt	cgt	gtt	gct	gcc	4656
Ala	Ile	Ile	Ala	His	Cys	Tyr	Glu	Phe	Arg	Asp	Phe	Arg	Val	Ala	Ala	
1540				1545				1550								
ttt	aag	ggg	gat	gat	tcg	gtg	gtc	ctc	tgt	agt	gac	tac	cga	cag	agc	4704
Phe	Lys	Gly	Asp	Asp	Ser	Val	Val	Leu	Cys	Ser	Asp	Tyr	Arg	Gln	Ser	
1555				1560				1565								
cgc	aat	gca	gct	gcc	tta	att	gct	ggc	tgt	ggg	ctc	aaa	ttg	aag	gtt	4752
Arg	Asn	Ala	Ala	Ala	Leu	Ile	Ala	Gly	Cys	Gly	Leu	Lys	Leu	Lys	Val	
1570				1575				1580								
gat	tac	cgc	cct	atc	ggg	ctg	tat	gct	ggg	gtg	gtg	gtg	gcc	ccc	ggg	4800
Asp	Tyr	Arg	Pro	Ile	Gly	Leu	Tyr	Ala	Gly	Val	Val	Val	Ala	Pro	Gly	
1585				1590				1595				1600				

ttg ggg aca ctg ccc gat gtg gtg cgt ttt gct ggt cgg ttg tct gaa Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly Arg Leu Ser Glu 1605 1610 1615	4848
aag aat tgg ggc ccc ggc ccg gaa cgt gct gag cag ctg cgt ctt gct Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala 1620 1625 1630	4896
gtc tgc gac ttc ctt cga ggg ttg acg aat gtt gcg cag gtc tgt gtt Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val 1635 1640 1645	4944
gat gtt gtg tcc cgt gtc tat gga gtc agc ccc ggg ctc gta cat aac Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn 1650 1655 1660	4992
ctt att ggc atg ctg cag acc atc gcc gat ggc aag gcc cac ttt aca Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr 1665 1670 1675 1680	5040
gag act att aaa cct gta ctt gat ctc aca aat tcc atc ata cag cgg Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg 1685 1690 1695	5088
gtg gaa tgaataacat gtcttttgca tcgcccattgg gatcacc atg cgc cct agg Val Glu Met Arg Pro Arg 1700	5143
gct gtt ctg ttg ttg ttc ctc atg ttt ctg cct atg ctg ccc gcg cca Ala Val Leu Leu Leu Phe Leu Met Phe Leu Pro Met Leu Pro Ala Pro 1705 1710 1715	5191
ccg gcc ggt cag ccg tct ggc cgt cgc cgt ggg cgg cgc agc ggc ggt Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg Arg Ser Gly Gly 1720 1725 1730	5239
gcc gcc ggt ggt ttc tgg agt gac agg gtt gat tct cag ccc ttc gcc Ala Gly Gly Gly Phe Trp Ser Asp Arg Val Asp Ser Gln Pro Phe Ala 1735 1740 1745 1750	5287
ctc ccc tat att cat cca acc aac ccc ttc gcc gcc gat gtc gtt tca Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser 1755 1760 1765	5335
caa ccc ggg gct gga act cgc cct cga cag ccg ccc cgc ccc ctc ggt Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly 1770 1775 1780	5383
tcc gct tgg cgt gac cag tcc aag cgc ccc tcc gtt gcc ccc cgt cgt Ser Ala Trp Arg Asp Gln Ser Lys Arg Pro Ser Val Ala Pro Arg Arg 1785 1790 1795	5431
cga tct acc cca gct ggg gct gcg ccg cta act gcc ata tca cca gcc Arg Ser Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Ile Ser Pro Ala 1800 1805 1810	5479

cct gat aca gct cct gta cct gat gtt gac tca cgt ggt gct att ttg	5527
Pro Asp Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu	
1815 1820 1825 1830	
cgc cgg cag tac aat ttg tct acg tcc ccg ctt aca tca tct gtt gct	5575
Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr Ser Ser Val Ala	
1835 1840 1845	
tct ggt act aat ctg gtt ctc tat gct gcc ccg ctg aac cct ctc ttg	5623
Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu Asn Pro Leu Leu	
1850 1855 1860	
cct ctt cag gat ggc acc aac act cat att atg gct act gag gca tct	5671
Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala Thr Glu Ala Ser	
1865 1870 1875	
aat tac gcc cag tat cgg gtt gtt cgg gct acg att cgt tat cgc ccg	5719
Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile Arg Tyr Arg Pro	
1880 1885 1890	
ttg gtg cca aat gct gtt ggt ggt tat gct atc tct att tct ttc tgg	5767
Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser Ile Ser Phe Trp	
1895 1900 1905 1910	
cct caa act aca act acc cct act tct gtt gac atg aat tct atc act	5815
Pro Gln Thr Thr Thr Pro Thr Ser Val Asp Met Asn Ser Ile Thr	
1915 1920 1925	
tct act gat gtc agg atc ttg gtc cag ccc ggt ata gcc tcc gag tta	5863
Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile Ala Ser Glu Leu	
1930 1935 1940	
gtc atc cct agt gaa cgc ctt cac tac cgc aac caa ggc tgg cgc tct	5911
Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln Gly Trp Arg Ser	
1945 1950 1955	
gtt gag acc acg ggt gtg gcc gaa gag gag gct acc tcc ggt ctg gta	5959
Val Glu Thr Thr Gly Val Ala Glu Glu Glu Ala Thr Ser Gly Leu Val	
1960 1965 1970	
atg ctt tgt att cat ggc tcc cct gtt aac tcc tac act aat aca cct	6007
Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr Thr Asn Thr Pro	
1975 1980 1985 1990	
tac acc ggt gca ttg ggg ctt ctt gat ttt gca tta gaa ctt gaa ttt	6055
Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu Glu Leu Glu Phe	
1995 2000 2005	
aga aat ttg aca ccc ggg aac act aac acc cgt gtt tcc cgg tat act	6103
Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val Ser Arg Tyr Thr	
2010 2015 2020	
agc aca gcc cgc cac cgg ctg cgc cgc ggt gct gat ggg acc gct gag	6151
Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp Gly Thr Ala Glu	
2025 2030 2035	
ctc acc acc aca gca gcc aca cgc ttc atg aag gat ttg cat ttt act	6199



Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu His Phe Thr	
2040	2045 2050
ggt acg aac ggc gtt ggt gag gtg ggt cgt ggt att gcc ctg act ctg	6247
Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala Leu Thr Leu	
2055	2060 2065 2070
ttt aat ctt gct gat acg ctt ctt ggt ggt tta ccg aca gaa ttg att	6295
Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile	
2075	2080 2085
tcg tcg gct ggg ggt caa ctg ttt tac tcc cgc cct gtt gtc tcg gcc	6343
Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala	
2090	2095 2100
aat ggc gag cca aca gta aag tta tac aca tct gtt gag aat gcg cag	6391
Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln	
2105	2110 2115
caa gac aag ggc atc acc att cca cac gac ata gat tta ggt gac tcc	6439
Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu Gly Asp Ser	
2120	2125 2130
cgt gtg gtt atc cag gat tat gat aac cag cac gaa caa gat cga cct	6487
Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp Arg Pro	
2135	2140 2145 2150
acc ccg tca cct gcc ccc tcc cgc cct ttc tca gtt ctt cgt gcc aat	6535
Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu Arg Ala Asn	
2155	2160 2165
gat gtt ttg tgg ctc tct ctc act gcc gct gag tac grc cag acc acg	6583
Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Xaa Gln Thr Thr	
2170	2175 2180
tat ggg tcg tcc acc aac cct atg tat gtc tct gat aca gtc acg ctt	6631
Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr Val Thr Leu	
2185	2190 2195
gtt aat gta gcc act ggt gct cag gct gtt gcc cgc tct ctt gac tgg	6679
Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser Leu Asp Trp	
2200	2205 2210
tct aaa gtt act ctg gat ggt cgc cct ctt act acc att cag cag tat	6727
Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr	
2215	2220 2225 2230
tct aag aaa ttt tat gtt ctc ccg ctt cgs ggg aag ctg tcc ttt tgg	6775
Ser Lys Lys Phe Tyr Val Leu Pro Leu Xaa Gly Lys Leu Ser Phe Trp	
2235	2240 2245
gag gct ggt acg acc aag gcc ggc tac ccg tat aat tat aat acc act	6823
Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr	
2250	2255 2260
gct agt gac caa att ttg att gag aac gcg gcc ggt cac cgt gtc gcc	6871
Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His Arg Val Ala	

2265	2270	2275	
att tct act tat acc act agt ttg ggt gcc ggc cct acc tcg aty tct			6919
Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro Thr Ser Xaa Ser			
2280	2285	2290	
gcg gtc ggt gta cta gct cca cat tcg gcc ctt gct gtt ctc gag gat			6967
Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val Leu Glu Asp			
2295	2300	2305	2310
act gtt gat tat cct gct cgt gcc cat act ttt gat gat ttc tgc ccg			7015
Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro			
	2315	2320	2325
gag tgt cgc acc ctt ggt ctg cag ggt tgt gca ttc caa tct act att			7063
Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile			
	2330	2335	2340
gct gaa ctt cag cgt ctt aaa atg aag gta ggt aaa acc cgg gag tct			7111
Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser			
	2345	2350	2355
taattaattc cttttgtgcc cccttcgcag ttctctttgg ctttatttct catttctgct			7171
ttccgcgctc cctggaaaaa aaaaaaaaaa a			7202

<210> 91  
 <211> 1698  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 174  
 <223> Xaa = Unknown or Other at position 363  
 <223> Xaa = Unknown or Other at position 1088  
 <223> Xaa = Unknown or Other at position 1131  
 <223> Xaa = Unknown or Other at position 1217  
 <223> Xaa = Unknown or Other at position 1389

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Ser	Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val
		20					25					30			
Gln	Thr	Glu	Ile	Leu	Ile	Asn	Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe
		35				40						45			
Arg	Pro	Glu	Val	Leu	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn
	50					55				60					
Glu	Leu	Glu	Gln	Tyr	Cys	Arg	Ala	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val
65				70					75					80	
Gly	Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Leu	His	Arg
			85				90						95		
Cys	Phe	Leu	Arg	Pro	Val	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala

			100					105					110		
Pro	Thr	Arg	Gly	Pro	Ala	Ala	Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly
		115					120					125			
Leu	Pro	Pro	Ala	Asp	Arg	Thr	Tyr	Cys	Phe	Asp	Gly	Phe	Ser	Arg	Cys
	130					135					140				
Ala	Phe	Ala	Ala	Glu	Thr	Gly	Val	Ala	Leu	Tyr	Ser	Leu	His	Asp	Leu
145				150						155					160
Trp	Pro	Ala	Asp	Val	Ala	Glu	Ala	Met	Ala	Arg	His	Gly	Xaa	Thr	Arg
			165						170					175	
Leu	Tyr	Ala	Ala	Leu	His	Leu	Pro	Pro	Glu	Val	Leu	Leu	Pro	Pro	Gly
			180					185					190		
Thr	Tyr	His	Thr	Thr	Ser	Tyr	Leu	Leu	Ile	His	Asp	Gly	Asp	Arg	Ala
		195					200					205			
Val	Val	Thr	Tyr	Glu	Gly	Asp	Thr	Ser	Ala	Gly	Tyr	Asn	His	Asp	Val
	210					215					220				
Ser	Ile	Leu	Arg	Ala	Trp	Ile	Arg	Thr	Thr	Lys	Ile	Val	Gly	Asp	His
225					230					235					240
Pro	Leu	Val	Ile	Glu	Arg	Val	Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu
				245					250					255	
Leu	Leu	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr
			260					265					270		
Pro	Arg	Ser	Thr	Glu	Val	Tyr	Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly
			275				280					285			
Ser	Pro	Ser	Leu	Phe	Pro	Ser	Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His
	290					295					300				
Ala	Val	Pro	Val	His	Ile	Trp	Asp	Arg	Leu	Met	Leu	Phe	Gly	Ala	Thr
305					310					315					320
Leu	Asp	Asp	Gln	Ala	Phe	Cys	Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg
				325					330					335	
Gly	Ile	Ser	Tyr	Lys	Val	Thr	Val	Gly	Ala	Leu	Val	Ala	Asn	Glu	Gly
			340					345					350		
Trp	Asn	Ala	Ser	Glu	Asp	Ala	Leu	Thr	Ala	Xaa	Ile	Thr	Ala	Ala	Tyr
	355						360					365			
Leu	Thr	Ile	Cys	His	Gln	Arg	Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys
	370					375					380				
Gly	Met	Arg	Arg	Leu	Gly	Val	Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg
385					390					395					400
Leu	Tyr	Ser	Trp	Leu	Phe	Glu	Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly
				405					410					415	
Arg	Gln	Leu	Gln	Phe	Tyr	Ala	Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly
			420					425					430		
Phe	His	Leu	Asp	Pro	Arg	Val	Leu	Val	Phe	Asp	Glu	Ser	Val	Pro	Cys
	435						440					445			
Arg	Cys	Arg	Thr	Phe	Leu	Lys	Lys	Val	Ala	Gly	Lys	Phe	Cys	Cys	Phe
	450														

Lys	Thr	Phe	Arg	Thr	Thr	Val	Val	Asp	Gly	Ala	His	Leu	Glu	Ala	Asn	
				565					570					575		
Gly	Pro	Glu	Gln	Tyr	Val	Leu	Ser	Phe	Asp	Ala	Ser	Arg	Gln	Ser	Met	
			580					585					590			
Gly	Ala	Gly	Ser	His	Ser	Leu	Thr	Tyr	Glu	Leu	Thr	Pro	Ala	Gly	Leu	
		595					600					605				
Gln	Val	Arg	Ile	Ser	Ser	Asn	Gly	Leu	Asp	Cys	Thr	Ala	Thr	Phe	Pro	
	610					615					620					
Pro	Gly	Gly	Ala	Pro	Ser	Ala	Ala	Pro	Gly	Glu	Val	Ala	Ala	Phe	Cys	
625					630					635					640	
Ser	Ala	Leu	Tyr	Arg	Tyr	Asn	Arg	Phe	Thr	Gln	Arg	His	Ser	Leu	Thr	
			645					650						655		
Gly	Gly	Leu	Trp	Leu	His	Pro	Glu	Gly	Leu	Leu	Gly	Ile	Phe	Pro	Pro	
		660						665					670			
Phe	Ser	Pro	Gly	His	Ile	Trp	Glu	Ser	Ala	Asn	Pro	Phe	Cys	Gly	Glu	
	675						680					685				
Gly	Thr	Leu	Tyr	Thr	Arg	Thr	Trp	Ser	Thr	Ser	Gly	Phe	Ser	Ser	Asp	
	690					695					700					
Phe	Ser	Pro	Pro	Glu	Ala	Ala	Ala	Pro	Ala	Met	Ala	Ala	Thr	Pro	Gly	
705					710					715					720	
Leu	Pro	His	Ser	Thr	Pro	Pro	Val	Ser	Asp	Ile	Trp	Val	Leu	Pro	Pro	
			725						730					735		
Pro	Ser	Glu	Glu	Phe	Gln	Val	Asp	Ala	Ala	Pro	Val	Pro	Pro	Ala	Pro	
		740						745					750			
Asp	Pro	Ala	Gly	Leu	Pro	Gly	Pro	Val	Val	Leu	Thr	Pro	Pro	Pro	Pro	
	755						760					765				
Pro	Pro	Val	His	Lys	Pro	Ser	Ile	Pro	Pro	Pro	Ser	Arg	Asn	Arg	Arg	
	770					775						780				
Leu	Leu	Tyr	Thr	Tyr	Pro	Asp	Gly	Ala	Lys	Val	Tyr	Ala	Gly	Ser	Leu	
785					790					795					800	
Phe	Glu	Ser	Asp	Cys	Asp	Trp	Leu	Val	Asn	Ala	Ser	Asn	Pro	Gly	His	
			805						810					815		
Arg	Pro	Gly	Gly	Gly	Leu	Cys	His	Ala	Phe	Tyr	Gln	Arg	Phe	Pro	Glu	
		820						825					830			
Ala	Phe	Tyr	Pro	Thr	Glu	Phe	Ile	Ile	His	Ala	Val	Ala	Pro	Asp	Tyr	Arg
	835						840						845			
Thr	Leu	Thr	Pro	Arg	Pro	Ile	Ile	His	Ala	Val	Ala	Pro	Asp	Tyr	Arg	
	850					855						860				
Val	Glu	Gln	Asn	Pro	Lys	Arg	Leu	Glu	Ala	Ala	Tyr	Arg	Glu	Thr	Cys	
865					870					875					880	
Ser	Arg	Arg	Gly	Thr	Ala	Ala	Tyr	Pro	Leu	Leu	Gly	Ser	Gly	Ile	Tyr	
			885						890					895		
Gln	Val	Pro	Val	Ser	Leu	Ser	Phe	Asp	Ala	Trp	Glu	Arg	Asn	His	Arg	
		900						905					910			
Pro	Gly	Asp	Glu	Leu	Tyr	Leu	Thr	Glu	Pro	Ala	Ala	Asn	Trp	Phe	Glu	
		915					920					925				
Ala	Asn	Lys	Pro	Ala	Gln	Pro	Val	Leu	Thr	Ile	Thr	Glu	Asp	Thr	Ala	
	930					935						940				
Arg	Thr	Ala	Asn	Leu	Ala	Leu	Glu	Ile	Asp	Ala	Ala	Thr	Glu	Val	Gly	
945					950					955					960	
Arg	Ala	Cys	Ala	Gly	Cys	Thr	Ile	Ser	Pro	Gly	Ile	Val	His	Tyr	Gln	
			965						970					975		
Phe	Thr	Ala	Gly	Val	Pro	Gly	Ser	Gly	Lys	Ser	Arg	Ser	Ile	Gln	Gln	
		980						985					990			
Gly	Asp	Val	Asp	Val	Val	Val	Val	Pro	Thr	Arg	Glu	Leu	Arg	Asn	Ser	
	995						1000					1005				
Trp	Arg	Arg	Arg	Gly	Phe	Ala	Ala	Phe	Thr	Pro	His	Thr	Ala	Ala	Arg	

1010		1015		1020
Val Thr Ile Gly Arg	Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro			
1025		1030		1040
Pro His Leu Leu Leu Leu	His Met Gln Arg Ala Ser Ser Val His Leu			
	1045		1050	1055
Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe Glu His Ala Gly				
	1060		1065	1070
Leu Val Pro Ala Ile Arg Pro Glu Leu Ala Pro Thr Ser Trp Trp Xaa				
	1075		1080	1085
Val Thr His Arg Cys Pro Ala Asp Val Cys Glu Leu Ile Arg Gly Ala				
	1090		1095	1100
Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg Ser Leu Phe Trp				
1105		1110		1120
Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Xaa Thr Gln Ala Ala Lys				
	1125		1130	1135
Ala Ala Asn Pro Gly Ala Ile Thr Val His Glu Ala Gln Gly Ala Thr				
	1140		1145	1150
Phe Thr Glu Thr Thr Ile Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile				
	1155		1160	1165
Gln Ser Ser Arg Ala His Ala Ile Val Ala Leu Thr Arg His Thr Glu				
	1170		1175	1180
Lys Cys Val Ile Leu Asp Ala Pro Gly Leu Leu Arg Glu Val Gly Ile				
1185		1190		1200
Ser Asp Val Ile Val Asn Asn Phe Phe Leu Ala Gly Gly Glu Val Gly				
	1205		1210	1215
Xaa His Arg Pro Ser Val Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu				
	1220		1225	1230
Gly Thr Leu Gln Ala Phe Pro Pro Ser Cys Gln Ile Ser Ala Tyr His				
	1235		1240	1245
Gln Leu Ala Glu Glu Leu Gly His Arg Pro Ala Pro Val Ala Ala Val				
	1250		1255	1260
Leu Pro Pro Cys Pro Glu Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln				
1265		1270		1280
Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu Leu Thr Asp Ile				
	1285		1290	1295
Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys Ala Val Leu Ser				
	1300		1305	1310
Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala				
	1315		1320	1325
His Ser Asp Val Arg Glu Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly				
	1330		1335	1340
Pro Val Gln Ala Thr Thr Cys Glu Leu Tyr Glu Leu Val Glu Ala Met				
1345		1350		1360
Val Glu Lys Gly Gln Asp Gly Ser Ala Val Leu Glu Leu Asp Leu Cys				
	1365		1370	1375
Asn Arg Asp Val Ser Arg Ile Thr Phe Phe Gln Lys Xaa Cys Asn Lys				
	1380		1385	1390
Phe Thr Thr Gly Glu Thr Ile Ala His Gly Lys Val Gly Gln Gly Ile				
	1395		1400	1405
Ser Ala Trp Ser Lys Thr Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg				
	1410		1415	1420
Ala Ile Glu Lys Glu Ile Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr				
1425		1430		1440
Gly Asp Ala Tyr Glu Glu Ser Val Phe Ala Ala Val Ser Gly Ala				
	1445		1450	1455
Gly Ser Cys Met Val Phe Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr				
	1460		1465	1470

Gln Asn Asn Phe Ser Leu Gly Leu Glu Cys Val Val Met Glu Glu Cys  
 1475 1480 1485  
 Gly Met Pro Gln Trp Leu Ile Arg Leu Tyr His Leu Val Arg Ser Ala  
 1490 1495 1500  
 Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys  
 1505 1510 1515 1520  
 His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr Val Trp Asn Met  
 1525 1530 1535  
 Ala Ile Ile Ala His Cys Tyr Glu Phe Arg Asp Phe Arg Val Ala Ala  
 1540 1545 1550  
 Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp Tyr Arg Gln Ser  
 1555 1560 1565  
 Arg Asn Ala Ala Ala Leu Ile Ala Gly Cys Gly Leu Lys Leu Lys Val  
 1570 1575 1580  
 Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val Val Ala Pro Gly  
 1585 1590 1595 1600  
 Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly Arg Leu Ser Glu  
 1605 1610 1615  
 Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala  
 1620 1625 1630  
 Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val  
 1635 1640 1645  
 Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn  
 1650 1655 1660  
 Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr  
 1665 1670 1675 1680  
 Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg  
 1685 1690 1695  
 Val Glu

<210> 92  
 <211> 660  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 481  
 <223> Xaa = Unknown or Other at position 542  
 <223> Xaa = Unknown or Other at position 595

<400> 92  
 Met Arg Pro Arg Ala Val Leu Leu Leu Phe Leu Met Phe Leu Pro Met  
 1 5 10 15  
 Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg  
 20 25 30  
 Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Ser Asp Arg Val Asp Ser  
 35 40 45  
 Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala  
 50 55 60  
 Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro  
 65 70 75 80  
 Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ser Lys Arg Pro Ser Val  
 85 90 95  
 Ala Pro Arg Arg Arg Ser Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala

			100					105					110			
Ile	Ser	Pro	Ala	Pro	Asp	Thr	Ala	Pro	Val	Pro	Asp	Val	Asp	Ser	Arg	
		115					120					125				
Gly	Ala	Ile	Leu	Arg	Arg	Gln	Tyr	Asn	Leu	Ser	Thr	Ser	Pro	Leu	Thr	
	130					135					140					
Ser	Ser	Val	Ala	Ser	Gly	Thr	Asn	Leu	Val	Leu	Tyr	Ala	Ala	Pro	Leu	
145					150					155					160	
Asn	Pro	Leu	Leu	Pro	Leu	Gln	Asp	Gly	Thr	Asn	Thr	His	Ile	Met	Ala	
				165					170					175		
Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Val	Arg	Ala	Thr	Ile	
		180						185					190			
Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	Ser	
		195					200					205				
Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	Met	
	210					215					220					
Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	Ile	
225					230					235					240	
Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	Gln	
				245					250					255		
Gly	Trp	Arg	Ser	Val	Glu	Thr	Thr	Gly	Val	Ala	Glu	Glu	Glu	Ala	Thr	
		260						265					270			
Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	Ser	Tyr	
		275					280					285				
Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	Leu	
	290					295					300					
Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	Arg	Val	
305					310					315					320	
Ser	Arg	Tyr	Thr	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	Asp	
				325					330					335		
Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	Asp	
		340						345					350			
Leu	His	Phe	Thr	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	Ile	
		355					360					365				
Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	Pro	
	370					375					380					
Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	Pro	
385					390					395					400	
Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val	
				405					410					415		
Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	Ile	Asp	
		420						425					430			
Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His	Glu	
		435														

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Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly
                    565                    570                    575
His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro
                    580                    585                    590
Thr Ser Xaa Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala
                    595                    600                    605
Val Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp
                    610                    615                    620
Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe
625                    630                    635                    640
Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys
                    645                    650                    655
Thr Arg Glu Ser
                    660

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<210> 93  
 <211> 122  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> ORF3 HEV US-1

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<400> 93
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1      5      10
Gly Leu Phe Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
20     25     30
His Arg Pro Val Ser Arg Leu Ala Val Ala Val Gly Gly Ala Ala Ala
35     40     45
Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser
50     55     60
Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met Ser Phe
65     70     75     80
His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser
85     90     95
Val Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro Pro Val
100    105    110
Val Asp Leu Pro Gln Leu Gly Leu Arg Arg
115    120

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<210> 94  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer US5P3S/20

<400> 94  
 tggcattact actgccattg

20

<210> 95  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence



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<220>
<223> Primer US5P45S/20

<400> 95
caattctgcc ttggcgaatg                                20

<210> 96
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer US5P296A

<400> 96
aggaaacacc gatgcagaac                                20

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer US5P243A/20

<400> 97
tccaacctcc aagcaacgac                                20

<210> 98
<211> 199
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Clone: 199con

<400> 98
caattctgcc ttggcgaatg ctgtggtggt tcggccggtt ctttctcgtg tgcaaaactga      60
gattcttatt aatttgatgc aaccccgcca gttggtcttc cgccctgagg tgctttggaa      120
tcacacctatc cagcgggtta tacataatga attagagcag tactgccggg cccgggctgg      180
tcgttgcttg gaggttgga                                199

<210> 99
<211> 25
<212> DNA
<213> Hepatitis E Virus

<220>
<223> JE orf1-s

<400> 99
gttctgcacg ggtgtttcct tagac                                25

<210> 100
<211> 26
<212> DNA
<213> Hepatitis E Virus

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&lt;220&gt;

&lt;223&gt; JE orf1-a

&lt;400&gt; 100

gaatcaggag atacgagggt gtgtgg

26

&lt;210&gt; 101

&lt;211&gt; 331

&lt;212&gt; DNA

&lt;213&gt; Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; us2-320

&lt;400&gt; 101

gttctgcac	ggtgtttcct	tagaccggc	ggccgagatg	ttcagcgctg	gtattctgcc	60
cctaccgctg	gtcctgcggc	caattgccgc	cgctccgctg	tgcgtggtct	ccccctgtc	120
gaccgcacct	attgttttga	tggattttcc	cgttgtgctt	ttgctgcaga	gaccggtgtg	180
gccctttact	ctttgcatga	cctttggcca	gctgatgttg	cagaggctat	ggcccgccat	240
gggatgacac	gcttatacgc	cgcactgcac	cttccccccg	aggtgctgct	accaccgggc	300
acctaccaca	caacctcgta	tctcctgatt	c			331

&lt;210&gt; 102

&lt;211&gt; 1186

&lt;212&gt; DNA

&lt;213&gt; Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; us2-1168

&lt;400&gt; 102

ctcactgtgt	ccgatagtgt	gttggttttt	gagcttacgg	atatagtcca	ctgccgtatg	60
gccgccccaa	gccagcgaaa	ggctgtttct	tcaacgcttg	tggggaggta	cggccgtagg	120
actaaattat	atgaggcggc	gcattcagat	gtccgtgagt	ccctagcgag	gtttatcccc	180
accatcggtg	ctgttcgggc	taccacatgt	gagctgtacg	agctgggtga	agccatggta	240
gagaagggtc	aggacggatc	tgccgtccta	gagctcgacc	tttgcaatcg	tgacgtctcg	300
cgcatcacat	ttttccaaaa	ggattgcaat	aagtttacia	ctggtgagac	tatcgcccat	360
ggcaagggtg	gccagggcac	atcggcctgg	agcaagacct	tctgtgctct	gtttggcccc	420
tggttcgcgc	ccattgaaaa	ggaaatattg	gccctactcc	cgcctaatat	cttttatggc	480
gacgcctatg	aggagtcagt	gtttgctgcc	gctgtgtccg	gggcaggggc	atgtatggta	540
tttgaaaatg	acttctcaga	gtttgacagt	accagaata	atctctctct	cggccttgag	600
tgtgtgggta	tggaggagtg	cggcatgccc	caatggttaa	ttaggttgta	ccatctggtc	660
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tctggtgagc	ctggtaccct	tctctggaac	actgtctgga	acatggcgat	tatagcacat	780
tgctaygagt	tccgtgactt	tcgtgttgcc	gccttcaagg	gtgatgattc	agtggctctc	840
tgtagtgact	accgacagrg	ccgtaacgcg	gctgccttaa	ttgcaggctg	tgggctcaaa	900
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gggacactgc	ccgatgtggt	gcgttttgcc	ggtcgggttat	ctgagaagaa	ttggggccct	1020
ggcccgagc	gtgctgagca	gctgcgtctt	gctgtttgtg	atttccttcg	agggttgacg	1080
aatgttgccg	aggtctgtgt	tgatgtttgt	tcccggtgtc	atggagttag	ccccgggctg	1140
gtacataacc	ttattggcat	gctgcagacc	atcgccgatg	gcaagg		1186

&lt;210&gt; 103

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Hepatitis E Virus

<220>  
 <223> JE hevdf2/3 s1  
  
 <400> 103  
 gttccgcttg gcgtgaccag tcc 23  
  
 <210> 104  
 <211> 23  
 <212> DNA  
 <213> Hepatitis E virus  
  
 <220>  
 <223> JE hevdf2/3 a1  
  
 <400> 104  
 gagtcaacat caggtacagg agc 23  
  
 <210> 105  
 <211> 130  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> us2-135  
  
 <400> 105  
 gttccgcttg gcgtgaccag tccagcgcc cctccgctgc cccccgtcgt cgatctgccc 60  
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 atgttgactc 130  
  
 <210> 106  
 <211> 26  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> JE hevdf1-s1  
  
 <400> 106  
 gatgtcattt tgtgttgctg ctcacc 26  
  
 <210> 107  
 <211> 23  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> hev216 a1  
  
 <400> 107  
 cgtcctacag cggcatggta ctg 23  
  
 <210> 108  
 <211> 564  
 <212> DNA  
 <213> Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; us2-563

&lt;400&gt; 108

tcacccatgc	cttatgttcc	ttaccctcgt	tcaacggagg	tgtatgtccg	gtctatattt	60
ggccctggcg	gctcccatc	cttgtttcca	tcagcctgct	ctactaaatc	tacctttcat	120
gctgtcccg	ttcacatctg	ggatcrgctc	atgctctttg	gtgccaccct	gracgatcag	180
gcgttctgct	gttcacggct	tatgacttac	ctccgtggta	ttagttataa	ggtcactgtc	240
ggtgcgcttg	tcgctaataa	ggggtggaac	gcctctgagg	atgctcttac	tgcagtgatc	300
actgcggcct	atctgacccat	ctgccatcag	cgttaccttc	gcacccaggc	gatttccaag	360
ggcatgcgcc	ggttggagg	tgagcatgct	cagaaattta	tcacaagact	ctacagctgg	420
ctatttgaga	agtctggccg	tgactacatc	cccggccgcc	agcttcaatt	ttatgcacaa	480
tgccgacggt	ggctttctgc	aggcttccac	ctaracccca	ggrtgcttgt	ctttgatgaa	540
tcagtaccat	gocgctgtag	gacg				564

&lt;210&gt; 109

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; USorf2.1'

&lt;400&gt; 109

gtggagctag	tacaccgacc	gcag	24
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&lt;210&gt; 110

&lt;211&gt; 678

&lt;212&gt; DNA

&lt;213&gt; Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; us2-667

&lt;400&gt; 110

cgcttcttgg	tggttttaccg	acagaattga	tttcgtcggc	tggggggccaa	ctgttttact	60
cccggccggt	tgtctcagcc	aatggcgagc	caacagtaaa	gttatataca	tctgttgaga	120
atgcgcagca	agacaagggc	atcaccattc	cacatgatat	agacctgggt	gactcccgtg	180
tggttatcca	ggattatgat	aaccagcayg	agcaagaccg	acctactccg	tcacctgccc	240
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ttacgcttgt	taatgtggct	actggtgctc	aggctgttgc	ccgctccctt	gattgggtcta	420
aagttactct	ggacggccgc	ccccttacta	ccattcagca	gtattctaag	acattttatg	480
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cttacaatta	taatactacc	gctagtgacc	aaattttgat	tgagaatgcg	gccggccacc	600
gtgtcgctat	ttccacctat	accactagct	taggtgccgg	tcctacctcg	atctctgcgg	660
tcggtgtact	agctccac					678

&lt;210&gt; 111

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; hev3301s

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 gtatgcgagc tcatccgtgg tgc 23

<210> 112  
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<220>  
 <223> JE hev167-a1

<400> 112  
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<210> 113  
 <211> 580  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> us2-579

<400> 113  
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 gctgccaacc ctgggtgcgat tacggttcac gaagctcagg gtgctacttt cacggagacc 180  
 acaattatag ccacggccga cgctaggggc ctcattcagt catcccgggc ccatgctata 240  
 gtgcgactca cccgccatac tgagaagtgt gttattttgg atgccccggg cttgttgcg 300  
 gaggtcggca tttcggatgt tattgtcaat aactttttcc ttgccgggtgg agaggtcggc 360  
 catcacccgc cttctgtgat acctcgcggc aatcctgac agaacctcg gactctacag 420  
 gcctttccgc cgtcatgtca gatcagtgt taccatcagt tggctgagga actaggtcat 480  
 cgccccggcc ctgtcgccgc cgtcttgccc ccttgccctg agcttgagca gggcctgctc 540  
 tatatgccac aagaactcac tgtgtccgat agtgtgttgg 580

<210> 114  
 <211> 26  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> HEV459 s1

<400> 114  
 cagaaattta tcacaagact ctacag 26

<210> 115  
 <211> 26  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> HEV459 s3

<400> 115  
 ctctacagtt ggctatttga gaagtc 26

<210> 116

<211> 25  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> JE1955a

<400> 116  
 ctataaagag ctgagcagaa ggcg

25

<210> 117  
 <211> 734  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> us2-733

<400> 117  
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 ttttatgcac aatgccgacg gtggctttct gcaggcttcc acctaraccc caggrtgctt 120  
 gtctttgatg aatcagtgcc atgccgttgc aggacgtttt tgaagaaggt cgcgggtaaa 180  
 ttctgctggt ttatgcggtg gctggggcag gagtgtacct gcttcttgga gccagccgag 240  
 ggtttagttg gtgatcaagg tcatgacaac gaggcctatg aagggttctga ggtcgaccca 300  
 gctgagcctg cacatcttga tgtctcgggg acttatgccg tccatgggca ccagcttgag 360  
 gccctctata gggcacttaa tgtcccacat gatattgccg ctcgagcctc ccgactaacg 420  
 gctactgttg agctcgttgc tagtcgggac cgcttagagt gccgcactgt acttggtaat 480  
 aagaccttcc ggacgacggt ggttgatggc gcccatcttg aagcgaatgg ccctgaggag 540  
 tatgttctgt catttgacgc ctctcgccag tctatggggg ccgggtcgca cagcctcact 600  
 tatgagctca cccctgccgg tctgcaggtg aagatttcat ctaatggtct ggattgcact 660  
 gccacattcc ccccyggtgg cgcccctagc gccgcgccgg gggaggtggc cgccttctgc 720  
 tcagctcttt atag 734

<210> 118  
 <211> 22  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> JE 2950mex s

<400> 118  
 gtgtcccgg ctctggcaag tc

22

<210> 119  
 <211> 22  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> JE us2-579-a2

<400> 119  
 cagggttggc agccttagca gc

22

<210> 120  
 <211> 483

<212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> us2-482  
  
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 acacagcggc ccgtgttact atcggccggc gcgttgtgat tgatgaggct ccatctctcc 180  
 caccgcacct gctgctgtta cacatgcagc gggcctcctc ggtccatctc cttggtgatc 240  
 caaaccagat tcctgctatt gattttgagc atgccggcct ggtcccccg atccgccccg 300  
 agcttgccgc aacgagctgg tggcacgtta cacaccgttg cccggccgat gtgtgcgagc 360  
 tcatacgtgg ggcctacccc aaaattcaga ccacgagccg tgtgctacgg tccctgtttt 420  
 ggaacgaacc ggccatcggc caaaagttag tttttacgca ggctgctaag gctgcccaacc 480  
 ctg 483  
  
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 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> JE 2600s  
  
 <400> 121  
 taacccaaag aggcttgagg ctgc 24  
  
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 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> us2-482-a1  
  
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 ccgctgtgtg aggtgtgaag gc 22  
  
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 <211> 23  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> us2-482-a2  
  
 <400> 123  
 gacgccagct gttacggagc tcc 23  
  
 <210> 124  
 <211> 431  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> us2-430

<400> 124  
 taacccaaag aggcttgagg ctgcgtaccg ggaaacttgc tcccgtcgtg gcaccgctgc 60  
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 ggaacgcaat caccgccccg gcgatgagct ttacttgaca gagcccgccg cagcctgggt 180  
 tgaggctaata aagccggcgc agccggcgct tactataact gaggacacgg cccgtacggc 240  
 caacctggca ttagagattg atgccgccac agaggttggc cgtgcttggt ccggctgcac 300  
 catcagcccc gggattgtgc actatcagtt taccgcccgg gtcccgggct caggcaagtc 360  
 aaggtccata caacagggag atgtcgatgt ggtgggtgtg cccacccggg agtcccgtaa 420  
 cagctggcgt c 431

<210> 125  
 <211> 22  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> us2-orf2/3 s1

<400> 125  
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<210> 126  
 <211> 25  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> HEVConsORF2-a1

<400> 126  
 cttgttctrtg ytggttrtca taatc 25

<210> 127  
 <211> 21  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> us2-orf2/3 s2

<400> 127  
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<210> 128  
 <211> 25  
 <212> DNA  
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<220>  
 <223> HEVConsORF2-a2

<400> 128  
 gttcrtgytg gtttrcataa tcctg 25

<210> 129  
 <211> 1020



<212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> us2-1019

<400> 129  
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 gtgctattct gcgcgcgcag tacaatttgt ccacgtcccc gctcacgtca tctgtcgctt 120  
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&lt;220&gt;

&lt;223&gt; us-84a

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Gln	Ala	Ala	Lys	Ala	Ala	Asn	Pro	Gly	Ala	Ile	Thr	Val	His	Glu	Ala	
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cag	ggg	gct	act	ttc	acg	gag	acc	aca	att	ata	gcc	acg	gcc	gac	gct	3557
Gln	Gly	Ala	Thr	Phe	Thr	Glu	Thr	Thr	Ile	Ile	Ala	Thr	Ala	Asp	Ala	
	1160					1165				1170						
agg	ggc	ctc	att	cag	tca	tcc	cgg	gcc	cat	gct	ata	gtc	gca	ctc	acc	3605
Arg	Gly	Leu	Ile	Gln	Ser	Ser	Arg	Ala	His	Ala	Ile	Val	Ala	Leu	Thr	
1175				1180				1185							1190	
cgc	cat	act	gag	aag	tgt	gtt	att	ttg	gat	gcc	ccc	ggc	ttg	ttg	cgc	3653
Arg	His	Thr	Glu	Lys	Cys	Val	Ile	Leu	Asp	Ala	Pro	Gly	Leu	Leu	Arg	
			1195					1200				1205				
gag	gtc	ggc	att	tcg	gat	gtt	att	gtc	aat	aac	ttt	ttc	ctt	gcc	ggg	3701
Glu	Val	Gly	Ile	Ser	Asp	Val	Ile	Val	Asn	Asn	Phe	Phe	Leu	Ala	Gly	
		1210					1215					1220				
gga	gag	gtc	ggc	cat	cac	cgc	cct	tct	gtg	ata	cct	cgc	ggc	aat	cct	3749
Gly	Glu	Val	Gly	His	His	Arg	Pro	Ser	Val	Ile	Pro	Arg	Gly	Asn	Pro	
		1225					1230				1235					
gat	cag	aac	ctc	ggg	act	cta	cag	gcc	ttt	ccg	ccg	tca	tgt	cag	atc	3797
Asp	Gln	Asn	Leu	Gly	Thr	Leu	Gln	Ala	Phe	Pro	Pro	Ser	Cys	Gln	Ile	
	1240					1245				1250						
agt	gct	tac	cat	cag	ttg	gct	gag	gaa	cta	ggg	cat	cgc	ccg	gcc	cct	3845
Ser	Ala	Tyr	His	Gln	Leu	Ala	Glu	Glu	Leu	Gly	His	Arg	Pro	Ala	Pro	
1255				1260				1265							1270	
gtc	gcc	gcc	gtc	ttg	ccc	cct	tgc	cct	gag	ctt	gag	cag	ggc	ctg	ctc	3893
Val	Ala	Ala	Val	Leu	Pro	Pro	Cys	Pro	Glu	Leu	Glu	Gln	Gly	Leu	Leu	

1275							1280							1285							
tat	atg	cca	caa	gaa	ctt	act	gtg	tcc	gat	agc	gtg	ctg	gtt	ttt	gag	3941					
Tyr	Met	Pro	Gln	Glu	Leu	Thr	Val	Ser	Asp	Ser	Val	Leu	Val	Phe	Glu						
1290				1295				1300													
ctt	acg	gat	ata	gtc	cac	tgc	cgt	atg	gcc	gcc	cca	agc	cag	cga	aag	3989					
Leu	Thr	Asp	Ile	Val	His	Cys	Arg	Met	Ala	Ala	Pro	Ser	Gln	Arg	Lys						
1305				1310				1315													
gct	gtt	ctc	tca	acg	ctt	gtg	ggg	agg	tac	ggc	cgt	agg	act	aaa	tta	4037					
Ala	Val	Leu	Ser	Thr	Leu	Val	Gly	Arg	Tyr	Gly	Arg	Arg	Thr	Lys	Leu						
1320				1325				1330													
tat	gag	gcg	gcg	cat	tca	gat	gtc	cgt	gag	tcc	cta	gcg	agg	ttt	atc	4085					
Tyr	Glu	Ala	Ala	His	Ser	Asp	Val	Arg	Glu	Ser	Leu	Ala	Arg	Phe	Ile						
1335				1340				1345				1350									
ccc	acc	atc	ggg	cct	gtt	cgg	gct	acc	aca	tgt	gag	ctg	tac	gag	ctg	4133					
Pro	Thr	Ile	Gly	Pro	Val	Arg	Ala	Thr	Thr	Cys	Glu	Leu	Tyr	Glu	Leu						
1355				1360				1365													
gtt	gaa	gcc	atg	gta	gag	aag	ggt	cag	gac	gga	tct	gcc	gtc	cta	gag	4181					
Val	Glu	Ala	Met	Val	Glu	Lys	Gly	Gln	Asp	Gly	Ser	Ala	Val	Leu	Glu						
1370				1375				1380													
ctc	gac	ctt	tgc	aat	cgt	gac	gtc	tgc	cgc	atc	aca	ttt	ttc	caa	aag	4229					
Leu	Asp	Leu	Cys	Asn	Arg	Asp	Val	Ser	Arg	Ile	Thr	Phe	Phe	Gln	Lys						
1385				1390				1395													
gat	tgc	aat	aag	ttt	aca	act	ggt	gag	act	atc	gcc	cat	ggc	aag	gtt	4277					
Asp	Cys	Asn	Lys	Phe	Thr	Thr	Gly	Glu	Thr	Ile	Ala	His	Gly	Lys	Val						
1400				1405				1410													
ggc	cag	ggc	ata	tgc	gcc	tgg	agc	aag	acc	ttc	tgt	gct	ctg	ttt	ggc	4325					
Gly	Gln	Gly	Ile	Ser	Ala	Trp	Ser	Lys	Thr	Phe	Cys	Ala	Leu	Phe	Gly						
1415				1420				1425				1430									
ccg	tgg	ttc	cgc	gcc	att	gaa	aag	gaa	ata	ttg	gcc	cta	ctc	ccg	cct	4373					
Pro	Trp	Phe	Arg	Ala	Ile	Glu	Lys	Glu	Ile	Leu	Ala	Leu	Leu	Pro	Pro						
1435				1440				1445													
aat	atc	ttt	tat	ggc	gac	gcc	tat	gag	gag	tca	gtg	ttt	gct	gcc	gct	4421					
Asn	Ile	Phe	Tyr	Gly	Asp	Ala	Tyr	Glu	Glu	Ser	Val	Phe	Ala	Ala	Ala						
1450				1455				1460													
gtg	tcc	ggg	gca	ggg	tca	tgt	atg	gta	ttt	gaa	aat	gac	ttc	tca	gag	4469					
Val	Ser	Gly	Ala	Gly	Ser	Cys	Met	Val	Phe	Glu	Asn	Asp	Phe	Ser	Glu						
1465				1470				1475													
ttt	gac	agt	acc	cag	aat	aat	ttc	tct	ctc	ggc	ctt	gag	tgt	gtg	gtt	4517					
Phe	Asp	Ser	Thr	Gln	Asn	Asn	Phe	Ser	Leu	Gly	Leu	Glu	Cys	Val	Val						
1480				1485				1490													
atg	gag	gag	tgc	ggc	atg	ccc	caa	tgg	tta	att	agg	ttg	tac	cat	ctg	4565					
Met	Glu	Glu	Cys	Gly	Met	Pro	Gln	Trp	Leu	Ile	Arg	Leu	Tyr	His	Leu						
1495				1500				1505				1510									

gtc cgg tca gcc tgg att ttg cag gcg ccg aag gag tct ctt aag ggg	4613
Val Arg Ser Ala Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly	
1515 1520 1525	
ttt tgg aag aag cac tct ggt gag cct ggt acc ctt ctc tgg aac act	4661
Phe Trp Lys Lys His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr	
1530 1535 1540	
gtc tgg aac atg gcg att ata gca cat tgc tay gag ttc cgt gac ttt	4709
Val Trp Asn Met Ala Ile Ile Ala His Cys Xaa Glu Phe Arg Asp Phe	
1545 1550 1555	
cgt gtt gcc gcc ttc aag ggt gat gat tca gtg gtc ctc tgt agt gac	4757
Arg Val Ala Ala Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp	
1560 1565 1570	
tac cga cag rgc cgt aac gcg gct gcc tta att gca ggc tgt ggg ctc	4805
Tyr Arg Gln Xaa Arg Asn Ala Ala Ala Leu Ile Ala Gly Cys Gly Leu	
1575 1580 1585 1590	
aaa ttg aag gtt gat tac cgc cct atc ggg cta tat gct gga gtg gtg	4853
Lys Leu Lys Val Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val	
1595 1600 1605	
gtg gcc ccc ggt ttg ggg aca ctg ccc gat gtg gtg cgt ttt gcc ggt	4901
Val Ala Pro Gly Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly	
1610 1615 1620	
cgg tta tct gag aag aat tgg ggc cct ggc ccg gag cgt gct gag cag	4949
Arg Leu Ser Glu Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln	
1625 1630 1635	
ctg cgt ctt gct gtt tgt gat ttc ctt cga ggg ttg acg aat gtt gcg	4997
Leu Arg Leu Ala Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala	
1640 1645 1650	
cag gtc tgt gtt gat gtt gtg tcc cgt gtc tat gga gtt agc ccc ggg	5045
Gln Val Cys Val Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly	
1655 1660 1665 1670	
ctg gta cat aac ctt att ggc atg ctg cag acc att gct gat ggc aag	5093
Leu Val His Asn Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys	
1675 1680 1685	
gcc cac ttt aca gar aat att aaa cct gtg ctt gac ctt aca aat tcc	5141
Ala His Phe Thr Xaa Asn Ile Lys Pro Val Leu Asp Leu Thr Asn Ser	
1690 1695 1700	
atc ata caa cgg gtg gaa tgaataacat gtcttttgca tcgccccatgg	5189
Ile Ile Gln Arg Val Glu	
1705	
gatacc atg cgc cct agg gct gtt ctg ttg ttg ctc ttc gtg ctt ttg	5238
Met Arg Pro Arg Ala Val Leu Leu Leu Leu Phe Val Leu Leu	
1710 1715 1720	

cct atg ctg ccc gcg cca ccg gcc ggc cag ccg tct ggc cgc cgt cgt	5286
Pro Met Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg	
1725 1730 1735	
ggg cgg cgc agc ggc ggt gcc ggc ggt ggt ttc tgg ggt gac agg gtt	5334
Gly Arg Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Gly Asp Arg Val	
1740 1745 1750	
gat tct cag ccc ttc gcc ctc ccc tat att cat cca acc aac ccc ttc	5382
Asp Ser Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe	
1755 1760 1765 1770	
gcc gcc gat gtc gtt tca caa ccc ggg gct gga act cgc cct cga cag	5430
Ala Ala Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln	
1775 1780 1785	
ccg ccc cgc ccc ctt ggy tcc gct tgg cgt gac cag tcc cag cgc ccc	5478
Pro Pro Arg Pro Leu Xaa Ser Ala Trp Arg Asp Gln Ser Gln Arg Pro	
1790 1795 1800	
tcc gct gcc ccc cgt cgt cga tct gcc cca gct ggg gct gcg ccg ctg	5526
Ser Ala Ala Pro Arg Arg Arg Ser Ala Pro Ala Gly Ala Ala Pro Leu	
1805 1810 1815	
act gcc gtg tca ccg gct cct gac aca gcc cct gta cct gat gtt gac	5574
Thr Ala Val Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val Asp	
1820 1825 1830	
tca cgt ggt gct att ctg cgc cgg cag tac aat ttg tcc acg tcc ccg	5622
Ser Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro	
1835 1840 1845 1850	
ctc acg tca tct gtc gct tcg ggt act aat ttg gtc ctc tat gct gcc	5670
Leu Thr Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala	
1855 1860 1865	
ccg ctg aat ccc ctc ttg cct ctc cag gat ggt acc aac act cat att	5718
Pro Leu Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile	
1870 1875 1880	
atg gct act gag gca tcc aat tat gcc cag tat ccg gtt gtt cga gct	5766
Met Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala	
1885 1890 1895	
aca atc cgt tat cgc ccg ctg gtg ccg aat gcc gtt ggt ggc tat gcc	5814
Thr Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala	
1900 1905 1910	
att tcc att tct ttc tgg ccc caa act aca act acc cct act tct gtc	5862
Ile Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val	
1915 1920 1925 1930	
gat atg aat tct att act tcc acy gat gtt agg att ttg gtt cag ccc	5910
Asp Met Asn Ser Ile Thr Ser Xaa Asp Val Arg Ile Leu Val Gln Pro	
1935 1940 1945	
ggt att gcc tcc gag cta gtc atc ccc agt gag cgc ctt cat tac cgt	5958

Gly	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	
			1950					1955					1960			
aat	caa	ggc	tgg	cgc	tct	gtt	gag	acc	acg	ggg	gtg	gct	gag	gag	gag	6006
Asn	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Thr	Gly	Val	Ala	Glu	Glu	Glu	
		1965					1970					1975				
gct	act	tcc	ggg	ctg	gta	atg	ctt	tgc	att	cat	ggc	tct	cct	gtt	aat	6054
Ala	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	
	1980					1985					1990					
tcc	tac	act	aat	aca	cct	tac	act	ggg	gcg	ctg	ggg	ctt	ctt	gat	ttt	6102
Ser	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	
1995					2000					2005					2010	
gca	cta	gag	ctt	gaa	ttt	agg	aat	ttg	aca	ccc	ggg	aac	acc	aac	acc	6150
Ala	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	
				2015					2020					2025		
cgt	gtt	tcc	cgg	tat	acc	agc	aca	gcc	cgc	cac	cgg	ctg	cgc	cgt	ggg	6198
Arg	Val	Ser	Arg	Tyr	Thr	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	
			2030					2035				2040				
gct	gat	ggg	act	gct	gag	ctt	act	acc	aca	gca	gcc	aca	cgt	ttc	atg	6246
Ala	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	
		2045					2050					2055				
aag	gac	ctg	cac	ttc	gct	ggc	acg	aat	ggc	gtt	ggg	gag	gtg	ggg	cgt	6294
Lys	Asp	Leu	His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	
	2060					2065					2070					
ggg	atc	gcc	ctg	aca	ctg	ttc	aat	ctc	gct	gat	acg	ctt	ctc	ggc	ggg	6342
Gly	Ile	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	
2075					2080					2085					2090	
tta	ccg	aca	gaa	ttg	att	tcg	tcg	gct	ggg	ggc	caa	ctg	ttt	tac	tcc	6390
Leu	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	
				2095					2100					2105		
cgc	ccg	gtt	gtc	tca	gcc	aat	ggc	gag	cca	aca	gta	aag	tta	tat	aca	6438
Arg	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	
				2110				2115					2120			
tct	gtt	gag	aat	gcg	cag	caa	gac	aag	ggc	atc	acc	att	cca	cat	gat	6486
Ser	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	
		2125					2130					2135				
ata	gac	ctg	ggg	gac	tcc	cgt	gtg	gtt	atc	cag	gat	tat	gat	aac	cag	6534
Ile	Asp	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	
	2140					2145					2150					
cay	gag	caa	gac	cga	cct	act	ccg	tca	cct	gcc	ccc	tct	cgc	ccc	ttc	6582
Xaa	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	
2155					2160					2165					2170	
tca	gtt	ctt	cgt	gcc	aat	gat	gtt	ttg	tgg	ctt	tcc	ctc	act	gcc	gct	6630
Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	

70/117

2175	2180	2185	
gag tat gac cag act acg tat ggg tcg tcc acc aac cct atg tat gtc Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val 2190 2195 2200			6678
tct gac aca gtt acg ctt gtt aat gtg gct act ggt gct cag gct gtt Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val 2205 2210 2215			6726
gcc cgc tcc ctt gat tgg tct aaa gtt act ctg gac ggc cgc ccc ctt Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu 2220 2225 2230			6774
act acc att cag cag tat tct aag aca ttt tat gtt ctc ccg ctc cgc Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg 2235 2240 2245 2250			6822
ggg aag ctg tcc ttt tgg gag gct ggc acg act aag gcc ggc tac cct Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro 2255 2260 2265			6870
tac aat tat aat act acc gct agt gac caa att ttg att gag aat gcg Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala 2270 2275 2280			6918
gcc ggc cac cgt gtc gct att tcc acc tat acc act agc tta ggt gcc Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala 2285 2290 2295			6966
ggt cct acc tcg atc tct gcg gtc ggc gta ctg gct cca cac tct gcc Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala 2300 2305 2310			7014
ctt gcc gtt ctt gag gat act att gat tac ccc gcc cgt gcc cat act Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr 2315 2320 2325 2330			7062
ttt gat gat ttt tgc ccg gag tgc cgt acc cta ggt ttg cag ggt tgt Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys 2335 2340 2345			7110
gca ttc cag tct act att gct gag ctc cag cgt tta aaa atg aag gta Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val 2350 2355 2360			7158
ggt aaa acc cgg gag tct taattaattc cttctgtgcc cccttcgtag Gly Lys Thr Arg Glu Ser 2365			7206
tttcttttcgc ttttatttct tattttctgct ttccgcgctc cctggaaaaa aaaaaaaaaa aaaaaaaaaa a			7266 7277

<210> 166  
 <211> 1708  
 <212> PRT  
 <213> Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; Xaa = Unknown or Other at position 322

&lt;223&gt; Xaa = Unknown or Other at position 331

&lt;223&gt; Xaa = Unknown or Other at position 445

&lt;223&gt; Xaa = Unknown or Other at position 448

&lt;223&gt; Xaa = Unknown or Other at position 634

&lt;223&gt; Xaa = Unknown or Other at position 646

&lt;223&gt; Xaa = Unknown or Other at position 811

&lt;223&gt; Xaa = Unknown or Other at position 1553

&lt;223&gt; Xaa = Unknown or Other at position 1578

&lt;223&gt; Xaa = Unknown or Other at position 1691

&lt;400&gt; 166

Met	Glu	Ala	His	Gln	Phe	Ile	Lys	Ala	Pro	Gly	Ile	Thr	Thr	Ala	Ile
1				5					10					15	
Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	Ser	Ala	Leu	Ala	Asn	Ala	Val
			20					25					30		
Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val	Gln	Thr	Glu	Ile	Leu	Ile	Asn
		35					40					45			
Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe	Arg	Pro	Glu	Val	Leu	Trp	Asn
	50					55					60				
His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu	Leu	Glu	Gln	Tyr	Cys	Arg
65				70					75						80
Ala	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val	Gly	Ala	His	Pro	Arg	Ser	Ile
			85						90					95	
Asn	Asp	Asn	Pro	Asn	Val	Leu	His	Arg	Cys	Phe	Leu	Arg	Pro	Val	Gly
			100					105					110		
Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala	Pro	Thr	Arg	Gly	Pro	Ala	Ala
		115					120					125			
Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly	Leu	Pro	Pro	Val	Asp	Arg	Thr
		130				135					140				
Tyr	Cys	Phe	Asp	Gly	Phe	Ser	Arg	Cys	Ala	Phe	Ala	Ala	Glu	Thr	Gly
145				150					155						160
Val	Ala	Leu	Tyr	Ser	Leu	His	Asp	Leu	Trp	Pro	Ala	Asp	Val	Ala	Glu
			165					170					175		
Ala	Met	Ala	Arg	His	Gly	Met	Thr	Arg	Leu	Tyr	Ala	Ala	Leu	His	Leu
			180					185					190		
Pro	Pro	Glu	Val	Leu	Leu	Pro	Pro	Gly	Thr	Tyr	His	Thr	Thr	Ser	Tyr
		195					200					205			
Leu	Leu	Ile	His	Asp	Gly	Asn	Arg	Ala	Val	Val	Thr	Tyr	Glu	Gly	Asp
		210				215					220				
Thr	Ser	Ala	Gly	Tyr	Asn	His	Asp	Val	Ser	Ile	Leu	Arg	Ala	Trp	Ile
225				230						235					240
Arg	Thr	Thr	Lys	Ile	Val	Gly	Asp	His	Pro	Leu	Val	Ile	Glu	Arg	Val
			245						250					255	
Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu	Leu	Leu	Thr	Ala	Ala	Pro	Glu
			260					265					270		

Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr	Pro	Arg	Ser	Thr	Glu	Val	Tyr
		275					280					285			
Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly	Ser	Pro	Ser	Leu	Phe	Pro	Ser
	290					295				300					
Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His	Ala	Val	Pro	Val	His	Ile	Trp
305					310					315					320
Asp	Xaa	Leu	Met	Leu	Phe	Gly	Ala	Thr	Leu	Xaa	Asp	Gln	Ala	Phe	Cys
			325						330					335	
Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg	Gly	Ile	Ser	Tyr	Lys	Val	Thr
		340					345					350			
Val	Gly	Ala	Leu	Val	Ala	Asn	Glu	Gly	Trp	Asn	Ala	Ser	Glu	Asp	Ala
	355						360				365				
Leu	Thr	Ala	Val	Ile	Thr	Ala	Ala	Tyr	Leu	Thr	Ile	Cys	His	Gln	Arg
	370					375				380					
Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys	Gly	Met	Arg	Arg	Leu	Glu	Val
385					390					395					400
Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg	Leu	Tyr	Ser	Trp	Leu	Phe	Glu
			405						410					415	
Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly	Arg	Gln	Leu	Gln	Phe	Tyr	Ala
		420						425					430		
Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly	Phe	His	Leu	Xaa	Pro	Arg	Xaa
	435						440				445				
Leu	Val	Phe	Asp	Glu	Ser	Val	Pro	Cys	Arg	Cys	Arg	Thr	Phe	Leu	Lys
	450					455				460					
Lys	Val	Ala	Gly	Lys	Phe	Cys	Cys	Phe	Met	Arg	Trp	Leu	Gly	Gln	Glu
465					470					475					480
Cys	Thr	Cys	Phe	Leu	Glu	Pro	Ala	Gly	Gly	Leu	Val	Gly	Asp	Gln	Gly
			485					490						495	
His	Asp	Asn	Glu	Ala	Tyr	Glu	Gly	Ser	Glu	Val	Asp	Pro	Ala	Glu	Pro
		500						505					510		
Ala	His	Leu	Asp	Val	Ser	Gly	Thr	Tyr	Ala	Val	His	Gly	His	Gln	Leu
	515						520					525			
Glu	Ala	Leu	Tyr	Arg	Ala	Leu	Asn	Val	Pro	His	Asp	Ile	Ala	Ala	Arg
	530					535				540					
Ala	Ser	Arg	Leu	Thr	Ala	Thr	Val	Glu	Leu	Val	Ala	Ser	Pro	Asp	Arg
545					550					555					560
Leu	Glu	Cys	Arg	Thr	Val	Leu	Gly	Asn	Lys	Thr	Phe	Arg	Thr	Thr	Val
			565					570						575	
Val	Asp	Gly	Ala	His	Leu	Glu	Ala	Asn	Gly	Pro	Glu	Glu	Tyr	Val	Leu
		580						585					590		
Ser	Phe	Asp	Ala	Ser	Arg	Gln	Ser	Met	Gly	Ala	Gly	Ser	His	Ser	Leu
	595						600					605			
Thr	Tyr	Glu	Leu	Thr	Pro	Ala	Gly	Leu	Gln	Val	Lys	Ile	Ser	Ser	Asn
	610					615					620				
Gly	Leu	Asp	Cys	Thr	Ala	Thr	Phe	Pro	Xaa	Gly	Gly	Ala	Pro	Ser	Ala
625					630					635					640
Ala	Pro	Gly	Glu	Val	Xaa	Ala	Phe	Cys	Ser	Ala	Leu	Tyr	Arg	Tyr	Asn
			645					650						655	
Arg	Phe	Thr	Gln	Arg	His	Ser	Leu	Thr	Gly	Gly	Leu	Trp	Leu	His	Pro
			660					665					670		
Glu	Gly	Leu	Leu	Gly	Ile	Phe	Pro	Pro	Phe	Ser	Pro	Gly	His	Ile	Trp
	675						680					685			
Glu	Ser	Ala	Asn	Pro	Phe	Cys	Gly	Glu	Gly	Thr	Leu	Tyr	Thr	Arg	Thr
	690					695					700				
Trp	Ser	Thr	Ser	Gly	Phe	Ser	Ser	Asp	Phe	Ser	Pro	Pro	Glu	Ala	Ala
705					710					715					720
Ala	Pro	Ala	Ser	Ala	Ala	Ala	Pro	Gly	Leu	Pro	Tyr	Pro	Thr	Pro	Pro



725					730					735					
Val	Ser	Asp	Ile	Trp	Val	Leu	Pro	Pro	Pro	Ser	Glu	Glu	Ser	His	Val
740					745					750					
Asp	Ala	Ala	Ser	Val	Pro	Ser	Val	Pro	Glu	Pro	Ala	Gly	Leu	Thr	Ser
755					760					765					
Pro	Ile	Val	Leu	Thr	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Val	Arg	Lys	Pro
770					775					780					
Ala	Thr	Ser	Pro	Pro	Pro	Arg	Thr	Arg	Arg	Leu	Leu	Tyr	Thr	Tyr	Pro
785					790					795					
Asp	Gly	Ala	Lys	Val	Tyr	Ala	Gly	Ser	Leu	Xaa	Glu	Ser	Asp	Cys	Asp
805					810					815					
Trp	Leu	Val	Asn	Ala	Ser	Asn	Pro	Gly	His	Arg	Pro	Gly	Gly	Gly	Leu
820					825					830					
Cys	His	Ala	Phe	Tyr	Gln	Arg	Phe	Pro	Glu	Ala	Phe	Tyr	Ser	Thr	Glu
835					840					845					
Phe	Ile	Met	Arg	Glu	Gly	Leu	Ala	Ala	Tyr	Thr	Leu	Thr	Pro	Arg	Pro
850					855					860					
Ile	Ile	His	Ala	Val	Ala	Pro	Asp	Tyr	Arg	Val	Glu	Gln	Asn	Pro	Lys
865					870					875					
Arg	Leu	Glu	Ala	Ala	Tyr	Arg	Glu	Thr	Cys	Ser	Arg	Arg	Gly	Thr	Ala
885					890					895					
Ala	Tyr	Pro	Leu	Leu	Gly	Ser	Gly	Ile	Tyr	Gln	Val	Pro	Val	Ser	Leu
900					905					910					
Ser	Phe	Asp	Ala	Trp	Glu	Arg	Asn	His	Arg	Pro	Gly	Asp	Glu	Leu	Tyr
915					920					925					
Leu	Thr	Glu	Pro	Ala	Ala	Ala	Trp	Phe	Glu	Ala	Asn	Lys	Pro	Ala	Gln
930					935					940					
Pro	Ala	Leu	Thr	Ile	Thr	Glu	Asp	Thr	Ala	Arg	Thr	Ala	Asn	Leu	Ala
945					950					955					
Leu	Glu	Ile	Asp	Ala	Ala	Thr	Glu	Val	Gly	Arg	Ala	Cys	Ala	Gly	Cys
965					970					975					
Thr	Ile	Ser	Pro	Gly	Ile	Val	His	Tyr	Gln	Phe	Thr	Ala	Gly	Val	Pro
980					985					990					
Gly	Ser	Gly	Lys	Ser	Arg	Ser	Ile	Gln	Gln	Gly	Asp	Val	Asp	Val	Val
995					1000					1005					
Val	Val	Pro	Thr	Arg	Glu	Leu	Arg	Asn	Ser	Trp	Arg	Arg	Arg	Gly	Phe
1010					1015					1020					
Ala	Ala	Phe	Thr	Pro	His	Thr	Ala	Ala	Arg	Val	Thr	Ile	Gly	Arg	Arg
1025					1030					1035					
Val	Val	Ile	Asp	Glu	Ala	Pro	Ser	Leu	Pro	Pro	His	Leu	Leu	Leu	Leu
1045					1050					1055					
His	Met	Gln	Arg	Ala	Ser	Ser	Val	His	Leu	Leu	Gly	Asp	Pro	Asn	Gln
1060					1065					1070					
Ile	Pro	Ala	Ile	Asp	Phe	Glu	His	Ala	Gly	Leu	Val	Pro	Ala	Ile	Arg
1075					1080					1085					
Pro	Glu	Leu	Ala	Pro	Thr	Ser	Trp	Trp	His	Val	Thr	His	Arg	Cys	Pro
1090					1095					1100					
Ala	Asp	Val	Cys	Glu	Leu	Ile	Arg	Gly	Ala	Tyr	Pro	Lys	Ile	Gln	Thr
1105					1110					1115					
Thr	Ser	Arg	Val	Leu	Arg	Ser	Leu	Phe	Trp	Asn	Glu	Pro	Ala	Ile	Gly
1125					1130					1135					
Gln	Lys	Leu	Val	Phe	Thr	Gln	Ala	Ala	Lys	Ala	Ala	Asn	Pro	Gly	Ala
1140					1145					1150					
Ile	Thr	Val	His	Glu	Ala	Gln	Gly	Ala	Thr	Phe	Thr	Glu	Thr	Thr	Ile
1155					1160					1165					
Ile	Ala	Thr	Ala	Asp	Ala	Arg	Gly	Leu	Ile	Gln	Ser	Ser	Arg	Ala	His
1170					1175					1180					

Ala Ile Val Ala Leu Thr Arg His Thr Glu Lys Cys Val Ile Leu Asp  
 1185 1190 1195 1200  
 Ala Pro Gly Leu Leu Arg Glu Val Gly Ile Ser Asp Val Ile Val Asn  
 1205 1210 1215  
 Asn Phe Phe Leu Ala Gly Gly Glu Val Gly His His Arg Pro Ser Val  
 1220 1225 1230  
 Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu Gly Thr Leu Gln Ala Phe  
 1235 1240 1245  
 Pro Pro Ser Cys Gln Ile Ser Ala Tyr His Gln Leu Ala Glu Glu Leu  
 1250 1255 1260  
 Gly His Arg Pro Ala Pro Val Ala Ala Val Leu Pro Pro Cys Pro Glu  
 1265 1270 1275 1280  
 Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln Glu Leu Thr Val Ser Asp  
 1285 1290 1295  
 Ser Val Leu Val Phe Glu Leu Thr Asp Ile Val His Cys Arg Met Ala  
 1300 1305 1310  
 Ala Pro Ser Gln Arg Lys Ala Val Leu Ser Thr Leu Val Gly Arg Tyr  
 1315 1320 1325  
 Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala His Ser Asp Val Arg Glu  
 1330 1335 1340  
 Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly Pro Val Arg Ala Thr Thr  
 1345 1350 1355 1360  
 Cys Glu Leu Tyr Glu Leu Val Glu Ala Met Val Glu Lys Gly Gln Asp  
 1365 1370 1375  
 Gly Ser Ala Val Leu Glu Leu Asp Leu Cys Asn Arg Asp Val Ser Arg  
 1380 1385 1390  
 Ile Thr Phe Phe Gln Lys Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr  
 1395 1400 1405  
 Ile Ala His Gly Lys Val Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr  
 1410 1415 1420  
 Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg Ala Ile Glu Lys Glu Ile  
 1425 1430 1435 1440  
 Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr Gly Asp Ala Tyr Glu Glu  
 1445 1450 1455  
 Ser Val Phe Ala Ala Ala Val Ser Gly Ala Gly Ser Cys Met Val Phe  
 1460 1465 1470  
 Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr Gln Asn Asn Phe Ser Leu  
 1475 1480 1485  
 Gly Leu Glu Cys Val Val Met Glu Glu Cys Gly Met Pro Gln Trp Leu  
 1490 1495 1500  
 Ile Arg Leu Tyr His Leu Val Arg Ser Ala Trp Ile Leu Gln Ala Pro  
 1505 1510 1515 1520  
 Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys His Ser Gly Glu Pro Gly  
 1525 1530 1535  
 Thr Leu Leu Trp Asn Thr Val Trp Asn Met Ala Ile Ile Ala His Cys  
 1540 1545 1550  
 Xaa Glu Phe Arg Asp Phe Arg Val Ala Ala Phe Lys Gly Asp Asp Ser  
 1555 1560 1565  
 Val Val Leu Cys Ser Asp Tyr Arg Gln Xaa Arg Asn Ala Ala Ala Leu  
 1570 1575 1580  
 Ile Ala Gly Cys Gly Leu Lys Leu Lys Val Asp Tyr Arg Pro Ile Gly  
 1585 1590 1595 1600  
 Leu Tyr Ala Gly Val Val Val Ala Pro Gly Leu Gly Thr Leu Pro Asp  
 1605 1610 1615  
 Val Val Arg Phe Ala Gly Arg Leu Ser Glu Lys Asn Trp Gly Pro Gly  
 1620 1625 1630  
 Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala Val Cys Asp Phe Leu Arg

	1635		1640		1645										
Gly	Leu	Thr	Asn	Val	Ala	Gln	Val	Cys	Val	Asp	Val	Val	Ser	Arg	Val
	1650					1655				1660					
Tyr	Gly	Val	Ser	Pro	Gly	Leu	Val	His	Asn	Leu	Ile	Gly	Met	Leu	Gln
1665					1670					1675				1680	
Thr	Ile	Ala	Asp	Gly	Lys	Ala	His	Phe	Thr	Xaa	Asn	Ile	Lys	Pro	Val
			1685					1690					1695		
Leu	Asp	Leu	Thr	Asn	Ser	Ile	Ile	Gln	Arg	Val	Glu				
		1700						1705							

<210> 167  
 <211> 660  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 84  
 <223> Xaa = Unknown or Other at position 230  
 <223> Xaa = Unknown or Other at position 447

<400> 167

Met	Arg	Pro	Arg	Ala	Val	Leu	Leu	Leu	Leu	Phe	Val	Leu	Leu	Pro	Met
1				5					10					15	
Leu	Pro	Ala	Pro	Pro	Ala	Gly	Gln	Pro	Ser	Gly	Arg	Arg	Arg	Gly	Arg
			20					25					30		
Arg	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Phe	Trp	Gly	Asp	Arg	Val	Asp	Ser
		35				40					45				
Gln	Pro	Phe	Ala	Leu	Pro	Tyr	Ile	His	Pro	Thr	Asn	Pro	Phe	Ala	Ala
	50					55					60				
Asp	Val	Val	Ser	Gln	Pro	Gly	Ala	Gly	Thr	Arg	Pro	Arg	Gln	Pro	Pro
65				70					75					80	
Arg	Pro	Leu	Xaa	Ser	Ala	Trp	Arg	Asp	Gln	Ser	Gln	Arg	Pro	Ser	Ala
			85					90					95		
Ala	Pro	Arg	Arg	Arg	Ser	Ala	Pro	Ala	Gly	Ala	Ala	Pro	Leu	Thr	Ala
			100					105					110		
Val	Ser	Pro	Ala	Pro	Asp	Thr	Ala	Pro	Val	Pro	Asp	Val	Asp	Ser	Arg
		115				120					125				
Gly	Ala	Ile	Leu	Arg	Arg	Gln	Tyr	Asn	Leu	Ser	Thr	Ser	Pro	Leu	Thr
	130					135					140				
Ser	Ser	Val	Ala	Ser	Gly	Thr	Asn	Leu	Val	Leu	Tyr	Ala	Ala	Pro	Leu
145				150					155					160	
Asn	Pro	Leu	Leu	Pro	Leu	Gln	Asp	Gly	Thr	Asn	Thr	His	Ile	Met	Ala
			165					170					175		
Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Val	Arg	Ala	Thr	Ile
		180				185						190			
Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	Ser
	195					200						205			
Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	Met
	210				215					220					
Asn	Ser	Ile	Thr	Ser	Xaa	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	Ile
225				230					235					240	
Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	Gln
			245					250					255		
Gly	Trp	Arg	Ser	Val	Glu	Thr	Thr	Gly	Val	Ala	Glu	Glu	Glu	Ala	Thr
		260						265					270		

Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	Ser	Tyr
		275					280					285			
Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	Leu
		290				295					300				
Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	Arg	Val
305					310					315					320
Ser	Arg	Tyr	Thr	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	Asp
				325					330					335	
Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	Asp
			340					345					350		
Leu	His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	Ile
		355					360					365			
Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	Pro
		370				375					380				
Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	Pro
385					390					395					400
Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val
				405					410					415	
Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	Ile	Asp
			420					425					430		
Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	Xaa	Glu
		435					440					445			
Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser	Val
		450				455					460				
Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu	Tyr
465					470					475					480
Asp	Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn	Pro	Met	Tyr	Val	Ser	Asp
				485					490					495	
Thr	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala	Arg
			500					505					510		
Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Thr	Thr
		515					520					525			
Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Tyr	Val	Leu	Pro	Leu	Arg	Gly	Lys
		530				535					540				
Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	Pro	Tyr	Asn
545					550					555					560
Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	Ile	Glu	Asn	Ala	Ala	Gly
				565					570					575	
His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly	Ala	Gly	Pro
			580					585					590		
Thr	Ser	Ile	Ser	Ala	Val	Gly	Val	Leu	Ala	Pro	His	Ser	Ala	Leu	Ala
		595				600						605			
Val	Leu	Glu	Asp	Thr	Ile	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe	Asp
		610				615					620				
Asp															

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<210> 168
<211> 122
<212> PRT
<213> Hepatitis E Virus
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<220>

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<223> us2 orf3

<223> Xaa = Unknown or Other at position 97

<400> 168

Met	Asn	Asn	Met	Ser	Phe	Ala	Ser	Pro	Met	Gly	Ser	Pro	Cys	Ala	Leu
1				5					10					15	
Gly	Leu	Phe	Cys	Cys	Ser	Ser	Cys	Phe	Cys	Leu	Cys	Cys	Pro	Arg	
			20				25					30			
His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Ala	Ala	Ala
		35				40					45				
Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser	Pro	Ser
	50				55				60						
Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met	Ser	Phe
65				70					75					80	
His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala	Pro	Leu
			85					90						95	
Xaa	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro	Pro	Val
		100					105					110			
Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg	Arg						
	115						120								

<210> 169

<211> 33

<212> PRT

<213> Hepatitis E Virus

<220>

<223> M 4-2

<400> 169

Ala	Asn	Gln	Pro	Gly	His	Leu	Ala	Pro	Leu	Gly	Glu	Ile	Arg	Pro	Ser
1				5				10						15	
Ala	Pro	Pro	Leu	Pro	Pro	Val	Ala	Asp	Leu	Pro	Gln	Pro	Gly	Leu	Arg
			20					25					30		

Arg

<210> 170

<211> 48

<212> PRT

<213> Hepatitis E Virus

<220>

<223> M 3-2e

<400> 170

Thr	Phe	Asp	Tyr	Pro	Gly	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1				5				10						15	
Glu	Cys	Arg	Ala	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Val
			20				25					30			
Ala	Glu	Leu	Gln	Arg	Leu	Lys	Val	Lys	Val	Gly	Lys	Thr	Arg	Glu	Leu
	35					40						45			

<210> 171

<211> 33

<212> PRT

<213> Hepatitis E Virus

<220>

<223> B 4-2

<400> 171

Ala	Asn	Pro	Pro	Asp	His	Ser	Ala	Pro	Leu	Gly	Val	Thr	Arg	Pro	Ser
1				5					10					15	
Ala	Pro	Pro	Leu	Pro	His	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Pro	Arg
			20					25					30		

Arg

<210> 172

<211> 48

<212> PRT

<213> Hepatitis E Virus

<220>

<223> B 3-2e

<400> 172

Thr	Leu	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1				5					10					15	
Glu	Cys	Arg	Pro	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Val
			20					25					30		
Ala	Glu	Leu	Gln	Arg	Leu	Lys	Met	Lys	Val	Gly	Lys	Thr	Arg	Glu	Leu
		35					40					45			

<210> 173

<211> 33

<212> PRT

<213> Hepatitis E Virus

<220>

<223> OFR3 (u4.2)

<400> 173

Asp	Ser	Arg	Pro	Ala	Pro	Ser	Val	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser
1				5					10					15	
Ala	Pro	Pro	Leu	Pro	Pro	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg
			20					25					30		

Arg

<210> 174

<211> 48

<212> PRT

<213> Hepatitis E Virus

<220>

<223> ORF2 (u3.2e)

<400> 174

Thr	Val	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1				5					10					15	
Glu	Cys	Arg	Thr	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Ile

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Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser

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<210> 175
<211> 327
<212> PRT
<213> Hepatitis E Virus
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<220>  
<223> US-1 SG3

<223> Xaa = Unknown or Other at position 148

<223> Xaa = Unknown or Other at position 209

<223> Xaa = Unknown or Other at position 262

	<400>						175									
Gly 1	Ala	Asp		Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe
					5					10				15		
Met	Lys	Asp		Leu	His	Phe	Thr	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly
				20					25					30		
Arg	Gly	Ile		Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly
		35						40					45			
Gly	Leu	Pro		Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr
	50						55					60				
Ser	Arg	Pro		Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr
65					70						75				80	
Thr	Ser	Val		Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His
					85					90				95		
Asp	Ile	Asp		Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn
				100					105					110		
Gln	His	Glu		Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro
		115						120					125			
Phe	Ser	Val		Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala
	130						135					140				
Ala	Glu	Tyr		Xaa	Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn	Pro	Met	Tyr
145					150						155				160	
Val	Ser	Asp		Thr	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala
					165					170					175	
Val	Ala	Arg		Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro
				180					185					190		
Leu	Thr	Thr		Ile	Gln	Gln	Tyr	Ser	Lys	Lys	Phe	Tyr	Val	Leu	Pro	Leu
		195						200					205			
Xaa	Gly	Lys		Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr
	210						215					220				
Pro	Tyr	Asn		Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	Ile	Glu	Asn
225					230						235				240	
Ala	Ala	Gly		His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly
					245					250					255	
Ala	Gly	Pro		Thr	Ser	Xaa	Ser	Ala	Val	Gly	Val	Leu	Ala	Pro	His	Ser
				260					265					270		
Ala	Leu	Ala		Val	Leu	Glu	Asp	Thr	Val	Asp	Tyr	Pro	Ala	Arg	Ala	His
		275						280					285			
Thr	Phe	Asp		Asp	Phe	Cys	Pro	Glu	Cys	Arg	Thr	Leu	Gly	Leu	Gln	Gly
	290						295					300				

80/117

Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys  
 305 310 315 320  
 Val Gly Lys Thr Arg Glu Ser  
 325

<210> 176  
 <211> 327  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> US-2 SG3

<223> Xaa = Unknown or Other at position 114

<400> 176  
 Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe  
 1 5 10 15  
 Met Lys Asp Leu His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly  
 20 25 30  
 Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly  
 35 40 45  
 Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr  
 50 55 60  
 Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr  
 65 70 75 80  
 Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His  
 85 90 95  
 Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn  
 100 105 110  
 Gln Xaa Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro  
 115 120 125  
 Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala  
 130 135 140  
 Ala Glu Tyr Asp Gln Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr  
 145 150 155 160  
 Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala  
 165 170 175  
 Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro  
 180 185 190  
 Leu Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu  
 195 200 205  
 Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr  
 210 215 220  
 Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn  
 225 230 235 240  
 Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly  
 245 250 255  
 Ala Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser  
 260 265 270  
 Ala Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His  
 275 280 285  
 Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly  
 290 295 300  
 Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys  
 305 310 315 320  
 Val Gly Lys Thr Arg Glu Ser



325

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<210> 177
<211> 21
<212> DNA
<213> Hepatitis E Virus

<220>
<223> HEVConsORF1-s2

<400> 177
ctgccytkgc gaatgctgtg g                                     21

<210> 178
<211> 24
<212> DNA
<213> Hepatitis E Virus

<220>
<223> HEVConsORF1-a2

<400> 178
ggcagwrtac carcgtgaa catc                                     24

<210> 179
<211> 294
<212> DNA
<213> Hepatitis E Virus

<220>
<223> z12-orf1 (G.S.)

<400> 179
tggcattact actgccattg agcaagctgc tctggctgcg gcccaattctg ccttggcgaa      60
tgctgtggtg gttcggccgt ttttatctcg ttacagact gagattctta ttaatttgat      120
gcaaccccg cagttggtct ttcgacctga ggtgttctgg aaccatccca tccaacgtgt      180
tatacataat gaattggagc agtactgccg ggcccgggcc ggctcgctgtc tggaaattgg      240
agcccatcca aggtcaatca atgataatcc taatgttctg catcggtgtt tcct          294

<210> 180
<211> 418
<212> DNA
<213> Hepatitis E Virus

<220>
<223> z12-orf1.con

<400> 180
ctggcattac tactgctatt gagcaagctg ctctgggtgc ggccaattct gccttggcga      60
atgctgtggt ggttcggccg tttttatctc gtttacagac tgagattctt attaatttga      120
tgcaaccccg acagttggtc tttcgacctg aggtgttctg gaaccatccc atccaacgtg      180
ttatacataa tgaattggag cagtactgcc gggcccgggc cggctcgctgt ctggaaattg      240
gagcccatcc aaggtcaatc aatgataatc ctaatgttct gcacgtgtgc tttttacgac      300
cggtcgggag ggaagttcag cgctgggtact ccgccccac ccgtggcccc gcggccaact      360
gccgcgggtc tgcgctgcgt ggtctcccc ccgtcgaccg cacttactgc ctcgatgg          418

<210> 181

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<211> 197  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> z12-orf2.con  
  
 <400> 181  
 gacagaatta atttcgctcgg ctgggggtca actgttctac tcccgcctg tcgtctcagc 60  
 caatggcgag ccgactgtca agttatacac atctgttgag aatgcacagc aggataaggg 120  
 gatagctatt ccacatgaca tagatttggg cgactctcgt ttggtaatcc aggattatga 180  
 taaccaacac gaacaag 197  
  
 <210> 182  
 <211> 25  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> HEVConsORF2/3-s1  
  
 <400> 182  
 gtatcggkyk gaatgaataa catgt 25  
  
 <210> 183  
 <211> 25  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> HEVConsORF2/3-a1  
  
 <400> 183  
 aggggttggt tggatgaata taggg 25  
  
 <210> 184  
 <211> 234  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> z12.orf23.con  
  
 <400> 184  
 gtatcggktt gaatgaataa catgttttgt gcatcgccca tgggatcacc atgcgccta 60  
 gggttgttct gttgttggtc ctctgttttc tgcctatgct gcccgcgcca ccggccggcc 120  
 agycgactgg ccgccgtcgt gggcgcgca gcggcggtgc cggcggtggt ttctgggggtg 180  
 acagggttga ttctcagccc ttccgacctc cctatatcca tccaaccaac ccct 234  
  
 <210> 185  
 <211> 890  
 <212> DNA  
 <213> Hepatitis E Virus  
  
 <220>  
 <223> z12-3p.race

<400> 185

gtcgtctcgg	ccaatggcga	gccgactgtc	aagttataca	catctgttga	gaatgcacag	60
caggataagg	ggatagctat	tccacatgac	atagatttgg	gcgactctcg	tttggtaatc	120
caggattacg	ataatcagca	cgagcaggac	cggcccaccc	cttcgcccgc	cccgtctcgt	180
cctttctcgg	tcctccgcgc	taatgatgct	ttgtggcttt	ctcttaccgc	tgctgagtat	240
gaccagacta	catatgggtc	gtccaccaac	ccgatgtatg	tctcagacac	tgttacattt	300
gtcaatgtgg	ccacaggggc	tcaggctgtc	gcccgtttct	ttgattgggc	taaagttacc	360
ctggacggcc	gccctcttac	taccatccag	cagtactcta	agacatttta	tgttctccca	420
cttcgcggga	agttatcttt	ttgggaggct	ggcacaacta	aagccgggta	cccttataat	480
tataacacaa	ctgctagtga	ccagattctg	attgaaaacg	cggctggcca	tcgtgtcgct	540
atatctactt	atactactag	cctgggcgcc	ggccctgtgt	cagtttctgc	ggttgggtgtg	600
ttagccccac	actcgagcct	tgctattctt	gaagacactg	ttgactatcc	ggcccgtgct	660
cacacttttg	atgacttctg	tccggaatgc	cgtgccctgg	gtctgcaggg	gtgtgctttt	720
caatctacta	tcgctgagct	ccagcgtctt	aaaatgaagg	taggcaaaac	ccgggagttt	780
taattaattc	ttcttggtgc	cccttcacgg	ttctcgcttt	atttctttct	tctgcctccc	840
gcgctccctg	gaaaaaaaaa	aaaaaaaaaa	gtactagtgc	acgcgtggcc		890

<210> 186

<211> 919

<212> DNA

<213> Hepatitis E Virus

<220>

<223> z12-3p.con

<400> 186

gacagaatta	atttcgtcgg	ctgggggtca	actgtttctac	tcccgcctcg	tcgtctcagc	60
caatggcgag	ccgactgtca	agttatacac	atctggttag	aatgcacagc	aggataaggg	120
gatagctatt	ccacatgaca	tagatttggg	cgactctcgt	ttggtaatcc	aggattacga	180
taatcagcac	gagcaggacc	ggcccacccc	ttcgcccgcg	ccgtctcgtc	ctttctcggg	240
cctccgcgct	aatgatgctt	tgtggctttc	tcttaccgct	gctgagtatg	accagactac	300
atatgggtcg	tccaccaacc	cgatgtatgt	ctcagacact	gttacatttg	tcaatgtggc	360
cacaggggct	caggctgtcg	cccgtttctt	tgattgggtc	aaagttaccc	tggaacggccg	420
ccctcttact	accatccagc	agtactctaa	gacattttat	gtttctcccac	ttcgcgggaa	480
gttatctttt	tgggaggctg	gcacaactaa	agccgggttac	ccttataatt	ataacacaac	540
tgctagtgc	cagattctga	ttgaaaacgc	ggctggccat	cgtgtcgcta	tatctactta	600
tactactagc	ctgggcgcgc	gccctgtgtc	agtttctcgc	gttggtgtgt	tagccccaca	660
ctcgagcctt	gctattcttg	aagacactgt	tgactatccg	gcccgtgctc	acacttttga	720
tgacttctgt	ccggaatgcc	gtgccctggg	tctgcagggg	tgtgcttttc	aatctactat	780
cgctgagctc	cagcgtctta	aaatgaaggt	aggcaaaacc	cgggagtttt	aattaattct	840
tcttggtgcc	ccttcacggg	tctcgcttta	tttctttctt	ctgcctcccg	cgctccctgg	900
aaaaaaaaaa	aaaaaaaaaa					919

<210> 187

<211> 138

<212> PRT

<213> Hepatitis E Virus

<220>

<223> z12-orf1.pep

<400> 187

Gly	Ile	Thr	Thr	Ala	Ile	Glu	Gln	Ala	Ala	Leu	Gly	Ala	Ala	Asn	Ser
1			5					10						15	
Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Leu	Gln
			20					25						30	
Thr	Glu	Ile	Leu	Ile	Asn	Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe	Arg

35							40					45				
Pro	Glu	Val	Phe	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu	
50							55					60				
Leu	Glu	Gln	Tyr	Cys	Arg	Ala	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Ile	Gly	
65					70			75				80				
Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Leu	His	Arg	Cys	
85					90				95							
Phe	Leu	Arg	Pro	Val	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala	Pro	
100					105				110							
Thr	Arg	Gly	Pro	Ala	Ala	Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly	Leu	
115			120				125									
Pro	Pro	Val	Asp	Arg	Thr	Tyr	Cys	Leu	Asp							
130						135										

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<210> 188
<211> 61
<212> PRT
<213> Hepatitis E Virus
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<220>  
<223> z12-orf2-5'.pep

<223> Xaa = Unknown or Other at position 25

<400> 188															
Met	Arg	Pro	Arg	Val	Val	Leu	Leu	Leu	Phe	Leu	Val	Phe	Leu	Pro	Met
1				5					10					15	
Leu	Pro	Ala	Pro	Pro	Ala	Gly	Gln	Xaa	Thr	Gly	Arg	Arg	Arg	Gly	Arg
			20					25					30		
Arg	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Phe	Trp	Gly	Asp	Arg	Val	Asp	Ser
		35					40					45			
Gln	Pro	Phe	Ala	Leu	Pro	Tyr	Ile	His	Pro	Thr	Asn	Pro			
	50					55					60				

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<210> 189
<211> 276
<212> PRT
<213> Hepatitis E Virus
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<220>  
<223> z12-orf2-3'.pep

	<400> 189														
Thr 1	Glu	Leu	Ile	Ser 5	Ser	Ala	Gly	Gly	Gln 10	Leu	Phe	Tyr	Ser 15	Arg	Pro
Val	Val	Ser	Ala 20	Asn	Gly	Glu	Pro	Thr 25	Val	Lys	Leu	Tyr	Thr 30	Ser	Val
Glu	Asn	Ala 35	Gln	Gln	Asp	Lys	Gly 40	Ile	Ala	Ile	Pro	His 45	Asp	Ile	Asp
Leu	Gly 50	Asp	Ser	Arg	Leu	Val 55	Ile	Gln	Asp	Tyr	Asp 60	Asn	Gln	His	Glu
Gln 65	Asp	Arg	Pro	Thr 70	Pro	Ser	Pro	Ala	Pro	Ser 75	Arg	Pro	Phe	Ser 80	Val
Leu	Arg	Ala	Asn	Asp 85	Ala	Leu	Trp	Leu	Ser 90	Leu	Thr	Ala	Ala 95	Glu	Tyr
Asp	Gln	Thr	Thr 100	Tyr	Gly	Ser	Ser	Thr 105	Asn	Pro	Met	Tyr	Val 110	Ser	Asp

```

Thr Val Thr Phe Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg
      115                      120                      125
Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr
      130                      135                      140
Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys
145                      150                      155                      160
Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn
      165                      170                      175
Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly
      180                      185                      190
His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro
      195                      200                      205
Val Ser Val Ser Ala Val Gly Val Leu Ala Pro His Ser Ser Leu Ala
      210                      215                      220
Ile Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp
225                      230                      235                      240
Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe
      245                      250                      255
Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys
      260                      265                      270
Thr Arg Glu Phe
      275

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<210> 190
<211> 74
<212> PRT
<213> Hepatitis E Virus

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<220>
<223> z12-orf3.pep

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<400> 190
Met Asn Asn Met Phe Cys Ala Ser Pro Met Gly Ser Pro Cys Ala Leu
 1      5      10      15
Gly Leu Phe Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
      20      25      30
His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala
      35      40      45
Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser
      50      55      60
Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro
65                      70

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<210> 191
<211> 408
<212> DNA
<213> Hepatitis E Virus

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<220>
<223> pJOorf3-29.seq

```

```

<400> 191
gaattcatga ataacatgtc ttttgcacgc cccatgggat caccatgcgc cctagggctg      60
ttctgttggt gctcttcgtg cttttgccta tgctgccgcg gccaccggcc agccagccgt      120
ctggccgcgc tcgtgggcgc cgcagcggcg gtgccggcgg tggtttctgg ggtgacaggg      180
ttgattctca gctcttcgcc ctcccctata ttcattccaa caacccttc gccgccgatg      240
tcgtttcaca acccgggggt ggaactcgcc ctgcacagcc gccccgcccc cttggctccg      300

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cttggcggtga	ccagtgcccag	cgccccctccg	ctgcccccccg	tcgtcgatct	gccccagctt	360
ggtctgcgcc	gcgactacaa	ggacgacgat	gacaagtaat	aaggatcc		408

<210> 192  
 <211> 1026  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> cksorf2m-2.seq

<400> 192						
gaattcatgg	gtgctgatgg	gactgctgag	cttactacca	cagcagccac	acgtttcatg	60
aaggacctgc	acttcgctgg	cacgaatggc	gttgggtgagg	tgggtcgtgg	tatcgccctg	120
acactgttca	atctcgctga	tacgcttctc	ggcgggtttac	cgacagaatt	gatttcgctg	180
gctggggggc	aactgtttta	ctcccgcccg	gttgtctcag	ccaatggcga	gccaacagta	240
aagttatata	catctgttga	gaatgcgcag	caagacaagg	gcataccat	tccacatgat	300
atagacctgg	gtgactcccg	tgtggttacc	caggattatg	ataaccagca	tgagcaagac	360
cgacctactc	cgtcacctgc	cccctctcgc	cccttctcag	ttcttcgtgc	caatgatgtt	420
ttgtggcttt	ccctcactgc	cgctgagtat	gaccagacta	cgtatgggtc	gtccaccaac	480
cctatgtatg	tctctgacac	agttacgctt	gttaatgtgg	ctactgggtc	tcaggctgtt	540
gcccgtctcc	ttgattggtc	taaagttact	ctggacggcc	gcccccttac	taccattcag	600
cagtattcta	agacatttta	tgttctcccg	ctccgcggga	agctgtcctt	ttgggaggct	660
ggcacgacta	aggccggcta	cccttacaat	tataatacta	ccgctagtga	ccaaattttg	720
attgagaatg	cggcgcggcca	ccgtgtcgtc	atttccacct	ataccactag	cttaggtgcc	780
ggtcctacct	cgatctctgc	ggtcggcgta	ctggctccac	actctgccct	tgccgttctt	840
gaggatacta	ttgattaccc	cgcccgtgcc	catacttttg	atgatttttg	cccggagtgc	900
cgtaaccctag	gtttgcaagg	ttgtgcattc	cagtcacta	ttgctgagct	ccagcgttta	960
aaaatgaagg	taggtaaaac	ccgggagctc	gactacaagg	acgacgatga	caagtaataa	1020
ggatcc						1026

<210> 193  
 <211> 1389  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> CKSORF32M-3.seq

<400> 193						
gaattcatga	ataacatgtc	ttttgcatcg	cccatgggat	caccatgcgc	cctagggctg	60
ttctgttggt	gctcttcgtg	cttttgcccta	tgctgcccgc	gccaccggcc	agccagccgt	120
ctggccgcgc	tcgtggggcg	cgtagcggcg	gtgccggcg	tggtttctgg	ggtgacagg	180
ttgattctca	gccccttcgc	ctcccctata	ttcatccaac	caacccttcc	gccgccgatg	240
tcgtttcaca	accgcgggct	ggaactcgcc	ctcgacagcc	gccccgcccc	cttggctccg	300
cttggcgtga	ccagtgcccag	cgcccctccg	ctgccccccg	tcgtcgatct	gccccagctt	360
ggtctgcgcc	gggtgctga	tgggactgct	gagcttacta	ccacagcagc	cacacgtttc	420
atgaaggacc	tgcacttcgc	tggcacgaat	ggcgttgggt	aggtgggtcg	tggtatcgcc	480
ctgacactgt	tcaatctcgc	tgatacgtt	ctcggcggtt	taccgacaga	attgatttcg	540
tcggctgggg	gccaactgtt	ttactcccgc	ccggttgtct	cagccaatgg	cgagccaaca	600
gtaaagttat	atacatctgt	tgagaatgcg	cagcaagaca	agggcatcac	cattccacat	660
gatatagacc	tgggtgactc	ccgtgtgggt	atccaggatt	atgataacca	gcatagacaa	720
gaccgacctc	ctccgtcacc	tgccccctct	cgccccctct	cagttcttcg	tgccaatgat	780
gttttggggc	tttccctcac	tgccgctgag	tatgaccaga	ctacgtatgg	gtcgtccacc	840
aaccctatgt	atgtctctga	cacagttacg	cttgttaatg	tggctactgg	tgctcaggct	900
gttgcgcgct	cccttgattg	gtctaaagtt	actctggacg	gcccggccct	tactaccatt	960
cagcagtatt	ctaagacatt	ttatgtttct	ccgctccgcg	ggaagctgtc	cttttggggg	1020

gctggcacga	ctaaggccgg	ctacccttac	aattataata	ctaccgctag	tgaccaaatt	1080
ttgattgaga	atgcggccgg	ccaccgtgtc	gctatttcca	cctataccac	tagcttaggt	1140
gccggtccta	cctcgatctc	tgcggtcggc	gtactggctc	cacactctgc	ccttgccggt	1200
cttgaggata	ctattgatta	ccccgcccg	gcccatactt	ttgatgattt	ttgcccggag	1260
tgccgtaccc	taggtttgca	gggttgtgca	ttccagtcta	ctattgctga	gctccagcgt	1320
ttaaaaatga	aggtaggtaa	aaccgcggag	tctgactaca	aggacgacga	tgacaagtaa	1380
taaggatcc						1389

<210> 194  
 <211> 408  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> plorf3-12.con

<400> 194						
gaattcatga	ataacatgtc	ttttgcatcg	cccatgggat	caccatgcgc	cctagggctg	60
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ctggccgcgg	tcgtggggcg	cgccagcgcg	gtgcccggcg	tggtttctgg	ggtgacaggg	180
ttgattctca	gcccttcgcc	ctccccata	ttcatccaac	caacccttc	gccgccgatg	240
tcgtttcaca	acccggggct	ggaactcgcc	ctcgacagcc	gccccgcccc	cttggtctcg	300
cttggcgtag	ccagtcccag	cgcccctccg	ctgccccccg	tcgtcgatct	gccccagctt	360
ggtctgcgcc	gcgactacaa	ggacgacgat	gacaagtaat	aaggatcc		408

<210> 195  
 <211> 1026  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> plorf2.2-6.seq

<400> 195						
gaattcatgg	gtgctgatgg	gactgctgag	cttactacca	cagcagccac	acgtttcatg	60
aaggacctgc	acttcgctgg	cacgaatggc	gttggtgagg	tgggtcgtgg	tatcgccctg	120
acactgttca	atctcgctga	tacgcttctc	ggcggtttac	cgacagaatt	gatttcgtcg	180
gctggggggc	aactgtttta	ctcccgcccc	gttgtctcag	ccaatggcga	gccaacagta	240
aagttatata	catctgttga	gaatgcgcag	caagacaagg	gcacacccat	tccacatgat	300
atagacctgg	gtgactcccg	tgtggttatc	caggattatg	ataaccagca	tgagcaagac	360
cgacctactc	cgtcacctgc	cccctctcgc	cccttctcag	ttcttcgtgc	caatgatgtt	420
ttgtggcttt	ccctcactgc	cgctgagtat	gaccagacta	cgtatgggtc	gtccaccaac	480
cctatgtatg	tctctgacac	agttacgctt	gttaatgtgg	ctactgggtc	tcaggctgtt	540
gcccgtctcc	ttgattggtc	taaagttact	ctggacggcc	gcccccttac	taccattcag	600
cagtattcta	agacatttta	tgttctcccc	ctccgcggga	agctgtcctt	ttgggaggct	660
ggcacgacta	aggccggcta	cccttacaat	tataatacta	ccgctagtga	ccaaattttg	720
attgagaatg	cgcccgccca	ccgtgtcgct	atttccacct	ataccactag	cttaggtgcc	780
ggtcctacct	cgatctctgc	ggtcggcgta	ctggctccac	actctgccct	tgccgttctt	840
gaggatacta	ttgattaccc	cgcccggtgc	catacttttg	atgatttttg	cccggagtgc	900
cgtaccctag	gtttgcaggg	ttgtgcattc	cagtctacta	ttgctgagct	ccagcgttta	960
aaaatgaagg	taggtaaaac	ccgggagctc	gactacaagg	acgacgatga	caagtaataa	1020
ggatcc						1026

<210> 196  
 <211> 1389  
 <212> DNA  
 <213> Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; PLORF32M-14-5.seq

&lt;400&gt; 196

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gaattcatga ataacatgtc ttttgcacgc cccatgggat caccatgcgc cctagggctg      60
ttctgttggt gctcttcgtg cttttgccta tgctgcccgc gccaccggcc agccagccgt      120
ctggccgccg tcgtggggcg cgtagcggcg gtgccggcgg tggtttctgg ggtgacaggg      180
ttgattctca gcccttcgcc ctcccctata ttcattccaa caacccttc gccgccgatg      240
tcgtttcaca acccggggct ggaactcgcc ctcgacagcc gccccgcccc cttggctccg      300
cttggcgtga ccagtcccag cgccccctcg ctgccccccg tcgtcgatct gcccagctt      360
ggtctgcgcc gcggtgctga tgggactgct gagcttacta ccacagcagc cacacgtttc      420
atgaaggacc tgcacttcgc tggcacgaat ggcgttggtg aggtgggtcg tggtatcgcc      480
ctgacactgt tcaatctcgc tgatacgctt ctcggcgggt taccgacaga attgatttcg      540
tcggctgggg gccaaactgt ttactccgcg ccggttgctc cagccaatgg cgagccaaca      600
gtaaagttat atacatctgt tgagaatgcg cagcaagaca agggcatcac cattccacat      660
gatatagacc tgggtgactc ccgtgtggtt atccaggatt atgataacca gcatgagcaa      720
gaccgacctt ctccgtcacc tgccccctct cgccccctct cagttcttcg tgccaatgat      780
gttttggtgg tttccctcac tgccgctgag tatgaccaga ctacgtatgg gtcgtccacc      840
aaccctatgt atgtctctga cacagttacg cttgttaatg tggctactgg tgctcaggct      900
gttgcccgtc cccttgattg gtctaaagt actctggacg gccgccccct tactaccatt      960
cagcagtatt ctaagacatt ttatgttctc ccgctccgcg ggaagctgtc cttttgggag     1020
gctggcacga ctaaggccgg ctacccttac aattataata ctaccgctag tgaccaaatt     1080
ttgattgaga atgcgggccg ccaccgtgtc gctattttcca cctataccac tagcttaggt     1140
gccggtccta cctcgatctc tgccgtcggc gtactggctc cacactctgc ccttgccgtt     1200
cttgaggata ctattgatta ccccgcccggt gcccatactt ttgatgattt ttgcccggag     1260
tgccgtacct taggtttgca gggttgtgca ttccagtcta ctattgctga gctccagcgt     1320
ttaaaaatga aggtaggtaa aaccggggag tctgactaca aggacgacga tgacaagtaa     1380
taaggatcc

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&lt;210&gt; 197

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; z12-orf3-5'.pep

&lt;223&gt; Xaa = Unknown or Other at position 37

&lt;400&gt; 197

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Met Asn Asn Met Phe Cys Ala Ser Pro Met Gly Ser Pro Cys Ala Leu
 1             5             10             15
Gly Leu Phe Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
      20             25             30
His Arg Pro Ala Xaa Arg Leu Ala Val Val Gly Gly Ala Ala Ala
      35             40             45
Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser
      50             55             60
Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro
65             70

```

&lt;210&gt; 198

&lt;211&gt; 63

&lt;212&gt; DNA

&lt;213&gt; Hepatitis E Virus



&lt;220&gt;

&lt;223&gt; Primer orf23p

&lt;400&gt; 198

tatatggatc cttattactt gtcacgctcg tcctttagt cagactcccg gggtttacct  
acc

60

63

&lt;210&gt; 199

&lt;211&gt; 338

&lt;212&gt; PRT

&lt;213&gt; Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; cksorf2m-2.pep

&lt;400&gt; 199

Glu	Phe	Met	Gly	Ala	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala		
1				5					10					15			
Thr	Arg	Phe	Met	Lys	Asp	Leu	His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly		
			20					25					30				
Glu	Val	Gly	Arg	Gly	Ile	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr		
		35				40					45						
Leu	Leu	Gly	Gly	Leu	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln		
	50					55				60							
Leu	Phe	Tyr	Ser	Arg	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val		
65				70						75					80		
Lys	Leu	Tyr	Thr	Ser	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr		
				85				90						95			
Ile	Pro	His	Asp	Ile	Asp	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp		
			100					105					110				
Tyr	Asp	Asn	Gln	His	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro		
		115					120					125					
Ser	Arg	Pro	Phe	Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser		
	130					135					140						
Leu	Thr	Ala	Ala	Glu	Tyr	Asp	Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn		
145				150						155					160		
Pro	Met	Tyr	Val	Ser	Asp	Thr	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly		
			165					170						175			
Ala	Gln	Ala	Val	Ala	Arg	Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp		
		180					185						190				
Gly	Arg	Pro	Leu	Thr	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Tyr	Val		
	195					200					205						
Leu	Pro	Leu	Arg	Gly	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Ser	Gly	Thr	Lys		
	210					215					220						
Ala	Gly	Tyr	Pro	Tyr	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu		
225				230						235				240			
Ile	Glu	Asn	Ala	Ala	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr		
		245						250						255			
Ser	Leu	Gly	Ala	Gly	Pro	Thr	Ser	Ile	Ser	Ala	Val	Gly	Val	Leu	Ala		
		260					265						270				
Pro	His	Ser	Ala	Leu	Ala	Val	Leu	Glu	Asp	Thr	Ile	Asp	Tyr	Pro	Ala		
	275						280					285					
Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro	Glu	Cys	Arg	Thr	Leu	Gly		
	290				295						300						
Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Ile	Ala	Glu	Leu	Gln	Arg	Leu		
305				310					315					320			
Lys	Met	Lys	Val	Gly	Lys	Thr	Arg	Glu	Ser	Asp	Tyr	Lys	Asp	Asp	Asp		

				325					330					335	
Asp Lys															
<210> 200 <211> 338 <212> PRT <213> Hepatitis E Virus  <220> <223> plorf2.2-6.pep  <400> 200															
Glu	Phe	Met	Gly	Ala	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala
1				5					10					15	
Thr	Arg	Phe	Met	Lys	Asp	Leu	His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly
			20					25					30		
Glu	Val	Gly	Arg	Gly	Ile	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr
		35					40					45			
Leu	Leu	Gly	Gly	Leu	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln
		50				55					60				
Leu	Phe	Tyr	Ser	Arg	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val
65					70					75				80	
Lys	Leu	Tyr	Thr	Ser	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr
				85					90					95	
Ile	Pro	His	Asp	Ile	Asp	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp
			100					105					110		
Tyr	Asp	Asn	Gln	His	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro
		115					120					125			
Ser	Arg	Pro	Phe	Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser
		130				135					140				
Leu	Thr	Ala	Ala	Glu	Tyr	Asp	Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn
145					150					155					160
Pro	Met	Tyr	Val	Ser	Asp	Thr	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly
				165					170					175	
Ala	Gln	Ala	Val	Ala	Arg	Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp
			180					185					190		
Gly	Arg	Pro	Leu	Thr	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Tyr	Val
		195					200					205			
Leu	Pro	Leu	Arg	Gly	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys
	210					215					220				
Ala	Gly	Tyr	Pro	Tyr	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu
225					230					235				240	
Ile	Glu	Asn	Ala	Ala	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr
				245					250					255	
Ser	Leu	Gly	Ala	Gly	Pro	Thr	Ser	Ile	Ser	Ala	Val	Gly	Val	Leu	Ala
			260					265					270		
Pro	His	Ser	Ala	Leu	Ala	Val	Leu	Glu	Asp	Thr	Ile	Asp	Tyr	Pro	Ala
		275					280					285			
Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro	Glu	Cys	Arg	Thr	Leu	Gly
	290					295					300				
Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Ile	Ala	Glu	Leu	Gln	Arg	Leu
305					310					315				320	
Lys	Met	Lys	Val	Gly	Lys	Thr	Arg	Glu	Ser	Asp	Tyr	Lys			

<210> 201  
 <211> 37  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Primer orf35p

<400> 201  
 tatatgaatt catgaataac atgtcttttg catcgcc

37

<210> 202  
 <211> 68  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Primer orf33p

<400> 202  
 tatatggatc cttattactt gtcacgctcg tcctttagt cgcggcgcag accaagctgg  
 ggcagatc

60  
 68

<210> 203  
 <211> 132  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> pJOorf3-29.pep

<400> 203  
 Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys  
 1 5 10 15  
 Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys  
 20 25 30  
 Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala  
 35 40 45  
 Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser  
 50 55 60  
 Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met  
 65 70 75 80  
 Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala  
 85 90 95  
 Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro  
 100 105 110  
 Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Asp Tyr Lys Asp  
 115 120 125  
 Asp Asp Asp Lys  
 130

<210> 204  
 <211> 132  
 <212> PRT  
 <213> Hepatitis E Virus

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<220>

<223> plorf3-12.pep

<400> 204

Glu	Phe	Met	Asn	Asn	Met	Ser	Phe	Ala	Ser	Pro	Met	Gly	Ser	Pro	Cys
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Ala	Leu	Gly	Leu	Phe	Cys	Cys	Cys	Ser	Ser	Cys	Phe	Cys	Leu	Cys	Cys
			20					25					30		
Pro	Arg	His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Ala
		35					40					45			
Ala	Ala	Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser
		50				55					60				
Pro	Ser	Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met
65					70					75				80	
Ser	Phe	His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala
			85						90					95	
Pro	Leu	Ala	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro
			100					105					110		
Pro	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg	Arg	Asp	Tyr	Lys	Asp
		115					120					125			
Asp	Asp	Asp	Lys												
		130													

<210> 205

<211> 48

<212> DNA

<213> Hepatitis E Virus

<220>

<223> Primer orf23

<400> 205

ctcagcagtc ccatcagcac cgcggcgcag accaagctgg ggcagatc

48

<210> 206

<211> 459

<212> PRT

<213> Hepatitis E Virus

<220>

<223> CKSORF32M-3.pep

<400> 206

Glu	Phe	Met	Asn	Asn	Met	Ser	Phe	Ala	Ser	Pro	Met	Gly	Ser	Pro	Cys
1				5					10					15	
Ala	Leu	Gly	Leu	Phe	Cys	Cys	Cys	Ser	Ser	Cys	Phe	Cys	Leu	Cys	Cys
			20					25					30		
Pro	Arg	His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Val
		35					40					45			
Ala	Ala	Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser
		50				55					60				
Pro	Ser	Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met
65					70					75				80	
Ser	Phe	His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala
			85						90					95	
Pro	Leu	Ala	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro
			100					105					110		

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Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Gly Ala Asp Gly
      115      120      125
Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu
      130      135      140
His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala
145      150      155      160
Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr
      165      170      175
Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val
      180      185      190
Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu
      195      200      205
Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu
      210      215      220
Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln
225      230      235      240
Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu
      245      250      255
Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Asp
      260      265      270
Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr
      275      280      285
Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser
      290      295      300
Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile
305      310      315      320
Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys Leu
      325      330      335
Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr
      340      345      350
Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His
      355      360      365
Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro Thr
      370      375      380
Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val
385      390      395      400
Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp
      405      410      415
Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln
      420      425      430
Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr
      435      440      445
Arg Glu Ser Asp Tyr Lys Asp Asp Asp Asp Lys
      450      455

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&lt;210&gt; 207

&lt;211&gt; 459

&lt;212&gt; PRT

&lt;213&gt; Hepatitis E Virus

&lt;220&gt;

&lt;223&gt; PLORF32M-14-5.pep

&lt;400&gt; 207

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Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys
 1      5      10      15
Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys

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			20					25					30		
Pro	Arg	His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Val
		35					40					45			
Ala	Ala	Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser
	50					55					60				
Pro	Ser	Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met
65					70					75					80
Ser	Phe	His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala
				85					90					95	
Pro	Leu	Ala	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro
			100					105					110		
Pro	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg	Arg	Gly	Ala	Asp	Gly
		115					120					125			
Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	Asp	Leu
	130					135					140				
His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	Ile	Ala
145					150					155					160
Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	Pro	Thr
				165					170					175	
Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	Pro	Val
			180					185					190		
Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val	Glu
		195					200					205			
Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	Ile	Asp	Leu
	210					215					220				
Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His	Glu	Gln
225					230					235					240
Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser	Val	Leu
				245					250					255	
Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu	Tyr	Asp
			260					265					270		
Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn	Pro	Met	Tyr	Val	Ser	Asp	Thr
		275					280					285			
Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala	Arg	Ser
	290					295					300				
Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Thr	Thr	Ile
305					310					315					320
Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Tyr	Val	Leu	Pro	Leu	Arg	Gly	Lys	Leu
				325					330					335	
Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	Pro	Tyr	Asn	Tyr
			340					345					350		
Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	Ile	Glu	Asn	Ala	Ala	Gly	His
		355					360					365			
Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly	Ala	Gly	Pro	Thr
	370														

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<211> 36
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Primer orf2mid5p

<400> 208
tatatgaatt catgggtgct gatgggactg ctgagc 36

<210> 209
<211> 418
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 1440o1.seq

<221> CDS
<222> (3)...(416)

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 209
ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gcc aat 47
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
1 5 10 15

tcc gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tcc cgt gtt 95
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val
20 25 30

caa act gat atc ctt att aac ctg atg caa ccc cgt cag ctt gtg ttc 143
Gln Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
35 40 45

cgg cct gaa gtt ctc tgg aac cat ccg atc cag cga gtt ata cat aat 191
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
50 55 60

gag ctg gaa caa tac tgt cga gcc cgc gct ggc cgc tgt ctt gag gtg 239
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
65 70 75

ggc gct cac cca agg tct att aat gat aac ccc aat gtt ctg cac cgg 287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
80 85 90 95

tgc ttt ctc cgc ccg gtt ggg aga gac gtc cag cgc tgg tat tcc gcc 335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
100 105 110

ccc act cgt ggt cca gcg gct aac tgc cgc cgt tct gcg cta cgc ggt 383

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Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly  
115 120 125

ttg ccc cct gtc gac cgc act tac tgt yty gat gg  
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp  
130 135

418

<210> 210  
<211> 138  
<212> PRT  
<213> Hepatitis E Virus

<220>  
<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 210  
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser  
1 5 10 15  
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln  
20 25 30  
Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg  
35 40 45  
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu  
50 55 60  
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly  
65 70 75 80  
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys  
85 90 95  
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro  
100 105 110  
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu  
115 120 125  
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp  
130 135

<210> 211  
<211> 197  
<212> DNA  
<213> Hepatitis E Virus

<220>  
<223> 1440o2.seq

<221> CDS  
<222> (2)...(196)

<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63



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<400> 211
g aca gaa ttr att tcg tcg gct gga ggt caa ctg ttc tac tcc cgc ccg      49
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
  1              5              10              15

ggt gtc tca gcc aat ggc gag ccg act gtt aag tta tac acc tct gtc      97
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
          20              25              30

gag aat gca cag cag gat aag ggc att gct ata cca cat gat ata gac      145
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
          35              40              45

tta ggg gat tcc cgt gtg gtt ata caa gat tat gay aac car cay gaa      193
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
          50              55              60

caa g
Gln
65      197
```

```
<210> 212
<211> 65
<212> PRT
<213> Hepatitis E Virus

<220>
<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63
```

```
<400> 212
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
  1              5              10              15
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
          20              25              30
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
          35              40              45
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
          50              55              60
Gln
65
```

```
<210> 213
<211> 418
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 2015-1.seq

<221> CDS
<222> (3)...(416)
```

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 213

ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gct aac	47
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn	
1 5 10 15	
tct gcc ttg gcg aat gct gtg gtg gtc cgg ccg ttc ctg tcc cgc act	95
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Thr	
20 25 30	
cag act gat att ctt att aat ttg atg caa ccc cgg caa ctt gta ttc	143
Gln Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe	
35 40 45	
cgc cct gag gtt ttg tgg aac cat ccg atc cag cga gtc ata cat aat	191
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn	
50 55 60	
gag ctg gag cag tat tgc cgt gct cgt gct ggt cgc tgc ctg gag gtt	239
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val	
65 70 75	
ggg gct cat cca aga tct atc aat gac aac cct aat gtt ctg cac cgg	287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg	
80 85 90 95	
tgt ttc ctc cgt ccg gtt ggg cga gac gta cag cgt tgg tat tct gcc	335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
cct act cgc ggc ccg gcg gct aat tgc cgc cgt tcc gcg tta cgt ggc	383
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
cta cct cct gtc gac cgc act tac tgt yty gat gg	418
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp	
130 135	

<210> 214

<211> 138

<212> PRT

<213> Hepatitis E Virus

<220>

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 214

```

Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser
 1          5          10          15
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Thr Gln
 20          25          30
Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg
 35          40          45
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
 50          55          60
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly
 65          70          75          80
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
 85          90          95
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
100          105          110
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
115          120          125
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
130          135

```

```

<210> 215
<211> 197
<212> DNA
<213> Hepatitis E Virus

```

```

<220>
<223> 2015o2.seq

<221> CDS
<222> (2)...(196)

```

```

<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

```

```

<400> 215
g aca gaa ttr att tcg tcg gct gga ggc cag ctc ttc tac tcc cgc cca      49
  Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
  1          5          10          15

gtc gtc tca gcc aat ggc gag ccg act gtt aaa ttg tat aca tcc gtc      97
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20          25          30

gag aat gcg cag cag gac aag ggc att gcc ata cca cat gat ata gat      145
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35          40          45

cta gga gat tcc cgc gtg gtt atc cag gat tat gay aac car cay gaa      193
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50          55          60

caa g      197
Gln
65

```

100/117

<210> 216  
<211> 65  
<212> PRT  
<213> Hepatitis E Virus

<220>  
<223> Xaa = Unknown or Other at position 3  
  
<223> Xaa = Unknown or Other at position 60  
  
<223> Xaa = Unknown or Other at positions 62-63

<400> 216  
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro  
1 5 10 15  
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val  
20 25 30  
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp  
35 40 45  
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu  
50 55 60  
Gln  
65

<210> 217  
<211> 251  
<212> DNA  
<213> Hepatitis E Virus

<220>  
<223> 14404-2.seq

<221> CDS  
<222> (3)...(251)  
<223> orf2

<223> orf3 from position 1 to position 165

<400> 217  
at att cat cca acc aac ccc ttt gcc tcc gac gtc gta tcg caa tcc 47  
Ile His Pro Thr Asn Pro Phe Ala Ser Asp Val Val Ser Gln Ser  
1 5 10 15  
ggg gct gga gct cgc cct cga cag ccg gcc cgc ccc ctc ggc tcc tct 95  
Gly Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ser  
20 25 30  
tgg cgt gac cag tcc cag cgc ccc ccc gct gtc ccc cgt cgt cga tct 143  
Trp Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Arg Ser  
35 40 45  
acc cca act ggg gct gcg ccg cta act gct gtt tca cca gcg cct gat 191  
Thr Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp  
50 55 60  
acg gcc cca gtc cct gat gtt gac tct cgt ggc gct atc ttg cgc cgg 239

101/117

Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg  
65 70 75

cag tat aac cta  
Gln Tyr Asn Leu  
80

251

<210> 218  
<211> 83  
<212> PRT  
<213> Hepatitis E Virus

<400> 218  
Ile His Pro Thr Asn Pro Phe Ala Ser Asp Val Val Ser Gln Ser Gly  
1 5 10 15  
Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ser Trp  
20 25 30  
Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Ser Thr  
35 40 45  
Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr  
50 55 60  
Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln  
65 70 75 80  
Tyr Asn Leu

<210> 219  
<211> 55  
<212> PRT  
<213> Hepatitis E Virus

<220>  
<223> 14404-2.seq orf3

<400> 219  
Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr Arg Asn Pro  
1 5 10 15  
Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser Ala Pro Leu  
20 25 30  
Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Ser Pro Val Val Asp Leu  
35 40 45  
Pro Gln Leu Gly Leu Arg Arg  
50 55

<210> 220  
<211> 251  
<212> DNA  
<213> Hepatits E Virus

<220>  
<223> 20154-2.seq

<221> CDS  
<222> (3)...(251)  
<223> orf2

102/117

<223> orf3 from position 1 to position 165

<400> 220

```
at att cat cca acc aac ccc ttt gcc gcc gac gtc gta tca caa ccc      47
  Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro
    1              5              10              15

ggg gct gga gct cgc cct cga cag ccg ccc cgc ccc ctc ggc tcc tct      95
Gly Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser
              20              25              30

tgg cgt gat cag tcc cag cgc ccc tcc gct gcc ccc cgt cgt cga tct      143
Trp Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Arg Ser
              35              40              45

acc cca gct ggg gct gcg ccg tta act gct gtt tcc cct gcg ccc gat      191
Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp
              50              55              60

acg gcc cca gtc ccc gac gtt gat tcc cgt ggt gcc atc ctg cgc cgg      239
Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg
              65              70              75

cag tat aac cta      251
Gln Tyr Asn Leu
  80
```

<210> 221

<211> 83

<212> PRT

<213> Hepatitis E Virus

<400> 221

```
Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro Gly
  1              5              10              15
Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser Trp
              20              25              30
Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Arg Ser Thr
              35              40              45
Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr
              50              55              60
Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln
  65              70              75              80
Tyr Asn Leu
```

<210> 222

<211> 55

<212> PRT

<213> Hepatitis E Virus

<220>

<223> 20154-2.seq orf3

<400> 222

```
Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr His Asn Pro
```

103/117

```

      1             5             10             15
Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser Ala Pro Leu
      20             25             30
Gly Val Ile Ser Pro Ser Ala Pro Pro Leu Pro Pro Val Val Asp Leu
      35             40             45
Pro Gln Leu Gly Leu Arg Arg
      50             55
```

<210> 223  
<211> 48  
<212> PRT  
<213> Hepatitis E Virus

<220>  
<223> US-2 3-2e

```

      1             5             10             15
Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro
      20             25             30
Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile
      35             40             45
Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser
```

<210> 224  
<211> 33  
<212> PRT  
<213> Hepatitis E Virus

<220>  
<223> US-2 4-2

```

      1             5             10             15
Asp Ser Arg Pro Ala Pro Leu Val Pro Leu Gly Val Thr Ser Pro Ser
      20             25             30
Ala Pro Pro Leu Pro Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg
Arg
```

<210> 225  
<211> 450  
<212> DNA  
<213> Hepatitis E Virus

<220>  
<223> 5p.pile {hpesvp}

```

      <400> 225
ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca actctgcctt      60
ggcgaatgct gtggtagtta ggccttttct ctctcaccag cagattgaga tcctcattaa      120
cctaatagcaa cctcgccagc ttgttttccg ccccgagggt ttctggaatc atcccatcca      180
gcgtgtcatc cataacgagc tggagcttta ctgccgcgcc cgctccggcc gctgtcttga      240
aattggcgcc catccccgct caataaatga taatcctaata gtggtccacc gctgcttcct      300
ccgccctggt gggcggtgat ttcagcgctg gtatactgct cccactcgcg ggccggctgc      360
taattgccgg cgttccgcgc tgcgcgggct tcccgtgctg gaccgcactt actgcctcga      420
cgggttttct ggctgtaact ttcccgcgca                                     450
```

<210> 226  
 <211> 450  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 5p.pile {hpeuigh}

<400> 226  
 ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca attctgccct 60  
 tgcgaatgct gtggtagtta ggctttttct ctctcaccag cagattgaga tccttattaa 120  
 cctaattgcaa cctcgccagc ttgttttccg ccccgagggt ttctggaacc accccatcca 180  
 gcgtgtcatc cataatgagc tggagcttta ctgtcgcgcc cgctccggcc gctgccttga 240  
 aattggtgcc caccctcgct caataaacga caatccta atgtgtccacc gctgcttcct 300  
 ccgccctgcc gggcgtgatg ttcagcgttg gtatactgct cctaccgcgc ggccggctgc 360  
 taattgccgg gggtccgcac tgcgcgggct ccccgctgct gaccgcactt actgcttcga 420  
 cgggttttct ggctgtaact ttcccgcga 450

<210> 227  
 <211> 450  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 5p.pile {hpea}

<400> 227  
 ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca actctgccct 60  
 tgcgaatgct gtggtagtta ggctttttct ctctcaccag cagattgaga tccttattaa 120  
 cctaattgcaa cctcgccagc ttgttttccg ccccgagggt ttctggaacc atcccatcca 180  
 gcgtgttatc cataatgagc tggagcttta ctgtcgcgcc cgctccggcc gctgcctcga 240  
 aattggtgcc ccccccgct caataaatga caatccta atgtgtccacc gttgcttcct 300  
 ccgtcctgcc gggcgtgatg ttcagcgttg gtatactgcc cctaccgcgc ggccggctgc 360  
 taattgccgg cggtccgcgc tgcgcgggct ccccgctgct gaccgcactt actgcttcga 420  
 cgggttttct ggctgtaact ttcccgcga 450

<210> 228  
 <211> 446  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 5p.pile {840455p}

<400> 228  
 cctggcatta ctactgccat tgagcaggct gctctggctg cggccaattc tgccttggcg 60  
 aatgctgtgg tgggtcgccc gtttttatct cgcgtgcaaa ccgagattct tattaatttg 120  
 atgcaacccc ggcagttggt tttccgccct gaggtacttt ggaatcacc tatccagcgg 180  
 gttatacata atgaattaga acagtactgc cgggctcggg ctggtcggtg cttggagggt 240  
 ggagctcacc caagatccat taatgacaac cccaacgttc tgcacgggtg tttccttaga 300  
 ccggttggcc gagatgttca gcgctggtac tctgccccca ccgcggccc tgcggcta at 360  
 tgccgcgcgt ccgcgttgcg tggctcccc cccgctgacc gcacttactg ctttgatgga 420  
 ttctcccggt gtgcttttgc tgcaga 446

<210> 229  
 <211> 450



<212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 5p.pile {hpenssp}

<400> 229  
 ggctcctggc atcactactg ctattgagca agcagctcta gcagcggcca actccgccct 60  
 tgcgaatgct gtggtgggtcc ggcctttcct ttcccatcag cagggttgaga tccttataaa 120  
 tctcatgcaa cctcggcagc tgggtgttcg tccctgaggtt ttttggaatc acccgattca 180  
 acgtgttata cataatgagc ttgagcagta ttgccgtgct cgctcggggtc gctgccttga 240  
 gattggagcc caccacgct ccattaatga taatcctaata gtcctccatc gctgctttct 300  
 ccaccccgct ggccgggatg ttcagcgctg gtacacagcc ccgactaggg gacctgcggc 360  
 gaactgtcgc cgctcggcac ttcggtgtct gccaccagcc gaccgcactt actgttttga 420  
 tggctttgcc ggctgccgtt ttgccgccga 450

<210> 230  
 <211> 450  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 5p Consensus

<221> variation  
 <222> (1)...(450)  
 <223> n = a or g or c or t/u, unknown or other in each  
 instance and is indicated in Figure 9

<400> 230  
 nnnncctggc atnactactg cnattgagca ngcngctctn gcngcggcca antcngccnt 60  
 ngcgaatgct gtggtngtnn ggcntttnt ntcncnnng cannngaga tncnatnaa 120  
 nntnatgcaa ccncgncagn tngtnttncg nccngaggtt ntntggaanc anccnatnca 180  
 ncngtnatn cataangann tngancnnta ntgncngcn cgnnnggnc gntgnntnga 240  
 nnttgngcn canccnngnt cnatnaanga naanccnaan gtntntcanc gntgnttnt 300  
 nnnccngnn ggncnggatg ttcagcgntg gtanncngcn ccnacnngng gncncngnc 360  
 naantgncn ngntcngcn tncngngnct nccnncngcn gaccgcactt actgnntnga 420  
 nggnttnncn ngntgnnnnt ttncngcnga 450

<210> 231  
 <211> 300  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {hpea} shown in Figure 9B

<400> 231  
 actgagtcag tgaagccagt gcttgacctg acaaattcaa ttctgtgtcg ggtggaatga 60  
 ataacatgct ttttgctgcg cccatgggtt cgcgaccatg cgccctcggc ctattttgct 120  
 gttgctcctc atgtttctgc ctatgctgcc cgcgccaccg cccggtcagc cgtctggccg 180  
 ccgtcgtggg cggcgcagcg gcggttccgg cgggtggttc tggggtgacc ggggttgattc 240  
 tcagcccttc gcaatccctt atattcatcc aaccaacccc ttgccecccg atgtcaccgc 300

<210> 232  
 <211> 300  
 <212> DNA

<213> Hepatitis E Virus

<220>

<223> 3p.pile {hpeuigh} shown in Figure 9B

<400> 232

actgagtcgg	tgaagccagt	gctcgacttg	acaaattcaa	tcctgtgtcg	ggtggaatga	60
ataacatgtc	ttttgctgcg	cccatggggt	ggcgaccatg	cgccctcggc	ctattttgct	120
gttgctcctc	atgtttctgc	ctatcgtgcc	cgcgccaccg	cccggtcagc	cgtctggccg	180
ccgtcgtggg	cggcgcagcg	gcggttccgg	cggtggtttc	tggggtgacc	gggttgattc	240
tcagcccttc	gcaatcccct	atattcatcc	aaccaacccc	ttcgcccccg	atgtcaccgc	300

<210> 233

<211> 300

<212> DNA

<213> Hepatitis E Virus

<220>

<223> 3p.pile {hpesvp} shown in Figure 9B

<400> 233

actgagtcag	taaaaccagt	gctcgacttg	acaaattcaa	tcttgtgtcg	ggtggaatga	60
ataacatgtc	ttttgctgcg	cccatggggt	cgcgaccatg	cgccctcggc	ctattttgtt	120
gctgctcctc	atgtttttgc	ctatgctgcc	cgcgccaccg	cccggtcagc	cgtctggccg	180
ccgtcgtggg	cggcgcagcg	gcggttccgg	cggtggtttc	tggggtgacc	gggttgattc	240
tcagcccttc	gcaatcccct	atattcatcc	aaccaacccc	ttcgcccccg	atgtcaccgc	300

<210> 234

<211> 300

<212> DNA

<213> Hepatitis E Virus

<220>

<223> 3p.pile {hpenssp} shown in Figure 9B

<400> 234

acagagtcctg	ttaagcctat	acttgacctt	acacactcaa	ttatgcaccg	gtctgaatga	60
ataacatgtg	gtttgctgcg	cccatggggt	cgccaccatg	cgccctaggc	ctcttttctt	120
gttgctcctc	ttgtttctgc	ctatgttgcc	cgcgccaccg	accggtcagc	cgtctggccg	180
ccgtcgtggg	cggcgcagcg	gcggtaccgg	cggtggtttc	tggggtgacc	gggttgattc	240
tcagcccttc	gcaatcccct	atattcatcc	aaccaacccc	tttgcgccag	acgttgccgc	300

<210> 235

<211> 297

<212> DNA

<213> Hepatitis E Virus

<220>

<223> 3p.pile {840453p} shown in Figure 9B

<400> 235

acagagacta	ttaaacctgt	acttgatctc	acaaattcca	tcatacagcg	ggtggaatga	60
ataacatgtc	ttttgcatcg	cccatgggat	caccatgcgc	cctagggctg	ttctgttggt	120
gttctcatg	tttctgccta	tgctgcccgc	gccaccggcc	ggtcagccgt	ctggccgctg	180
ccgtgggcgg	cgagcggcg	gtgccggcgg	tggtttctgg	agtgacaggg	ttgattctca	240
gcccttcgcc	ctcccctata	ttcatccaac	caacccttc	gccgccgatg	tcgttttc	297

<210> 236  
 <211> 300  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p Consensus shown in Figure 9B

<221> variation  
 <222> (3)...(300)  
 <223> n = a or g or c or t/u, unknown or other in each instance and is indicated in Figure 9B

<400> 236  
 acngagncnn tnaanccnnt nctngannntn acanantcna tnntnnnnncg gnnngaattga 60  
 ataacatgtn ntttgenncg cccatgggnt nnnnaccatg cgcctnggn ctnttntgnt 120  
 gntgntcctc ntgtttntgc ctatnntgcc cgcgccaccg nccggtcagc cgtctggccg 180  
 ncgncgtggg cggcgcagcg gcggtncgg cggtggtttc tggngtgacn gggttgattc 240  
 tcagcccttc genntccct atattcatcc aaccaacccc ttngccneng angtnnnnnc 300

<210> 237  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {hpea} shown in Figure 9C

<400> 237  
 agcgcttacc ctgtttaacc ttgctgacac cctgcttggc ggtctaccga cagaattgat 60  
 ttcgtcggct ggtggccagc tgttctactc tcgccccgtc gtctcagcca atggcgagcc 120  
 gactgttaag ctgtatacat ctgtggagaa tgctcagcag gataagggta ttgcaatccc 180  
 gcatgacatc gacctcgggg aatcccgtgt agttattcag gattatgaca accaacaatga 240  
 gcaggaccga 250

<210> 238  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {hpeuigh} shown in Figure 9C

<400> 238  
 agcgcttacc ctgtttaacc ttgctgacac cctgcttggc ggtctaccga cagaattgat 60  
 ttcgtcggct ggtggccagc tgttctactc tcgccccgtc gtctcagcca atggcgagcc 120  
 gactgttaag ctgtatacat ctgttagagaa tgctcagcag gataagggta ttgcaatccc 180  
 gcatgacatc gacctcgggg aatctcgagt tgttattcag gattatgaca accaacaatga 240  
 gcaggaccgg 250

<210> 239  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {hpesvp} shown in Figure 9C

<400> 239  
 agccctcacc ctgttcaacc ttgctgacac tctgcttggc ggcttgccga cagaattgat 60  
 ttcgtcggct ggtggccagc tgttctactc ccgtcccgtt gtctcagcca atggcgagcc 120  
 gactgttaag ttgtatacat ctgtagagaa tgctcagcag gataagggtg ttgcaatccc 180  
 gcatgacatt gacctcggag aatctcgtgt ggttattcag gattatgata accaacaatga 240  
 acaagatcgg 250

<210> 240  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {hpenssp} shown in Figure 9C

<400> 240  
 agctctaaca ttacttaacc ttgctgacac gctcctcggc gggctcccga cagaattaat 60  
 ttcgtcggct ggcgggcaac tgttttattc ccgcccgtt gtctcagcca atggcgagcc 120  
 aaccgtgaag ctctatacat cagtggagaa tgctcagcag gataagggtg ttgctatccc 180  
 ccacgatatc gatcttgggtg attcgcgtgt ggtcattcag gattatgata accagcatga 240  
 gcaggatcgg 250

<210> 241  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p.pile {840453p} shown in Figure 9C

<400> 241  
 tgccctgact ctgtttaatc ttgctgatac gcttcttggg ggtttaccga cagaattgat 60  
 ttcgtcggct ggggggtcaac tgttttactc ccgccctgtt cagaattgat ttcgtcggct 120  
 ggggggtcaac tgttttactc ccgccctgtt tgccgagcaa gacaaggga tcaccattcc 180  
 acacgacata gatttaggtg actcccgtgt ggttatccag gattatgata accagcacga 240  
 acaagatcga 250

<210> 242  
 <211> 250  
 <212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> 3p Consensus shown in Figure 9C

<221> variation  
 <222> (1)...(250)  
 <223> n = a or g or c or t/u, unknown or other at each  
 instance and is indicated in Figure 9C

<400> 242  
 ngcnctnact ntnntnaanc ttgctganac nctnctnggn ggnntnccga cagaattnat 60  
 ttcgtcggct ggnngncanc tgtntantc ncgnccngtn gtctcngcca atggcgagcc 120  
 nacngtnaag ntntanacat cngtnagagaa tgcnacgcan ganaagggnn tnnnatncc 180  
 ncanganatn ganntnggng antcncngnt ngtnatncag gattatgana accancanga 240  
 ncanganagn 250

```

<210> 243
<211> 418
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Aulo1-wlabolp1.pat

<221> CDS
<222> (3)...(416)

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 243
ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aat      47
  Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
    1             5             10             15

tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tcc cgt gtg      95
  Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val
                20             25             30

cag act gag atc ctt att aac ttg atg caa cct cgg cag ctg gtg ttc      143
  Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
                35             40             45

cga cct gag gtg ctt tgg aat cat ccc att cag cgg gtt atc cat aat      191
  Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
                50             55             60

gag tta gaa caa tac tgc cgg gcc cgg gcc ggc cgt tgc cta gag gtg      239
  Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
                65             70             75

ggg gcc cac cca agg tcc att aac gat aac ccc aat gtt ttg cac cgg      287
  Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
                80             85             90             95

tgt ttt ctg cga ccg gtc ggg agg gat gtt cag cgc tgg tac tct gcc      335
  Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
                100             105             110

ccc acc cgc ggc cct gcg gct aac tgc cgc cgc tcc gct ttg cgt ggc      383
  Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly
                115             120             125

ctt ccc ccc gtc gac cgc act tac tgt yty gat gg                      418
  Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
                130             135

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<210> 244

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<211> 138  
<212> PRT  
<213> Hepatitis E Virus

<220>  
<223> Xaa = Unknown or Other at position 2  
  
<223> Xaa = Unknown or Other at position 5  
  
<223> Xaa = Unknown or Other at position 137

<400> 244  
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Asn Ser  
1 5 10 15  
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln  
20 25 30  
Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg  
35 40 45  
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu  
50 55 60  
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly  
65 70 75 80  
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys  
85 90 95  
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro  
100 105 110  
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu  
115 120 125  
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp  
130 135

<210> 245  
<211> 197  
<212> DNA  
<213> Hepatitis E Virus

<220>  
<223> Aulo2-wlao2.pat  
  
<221> CDS  
<222> (2)...(196)  
  
<223> Xaa = Unknown or Other at position 3  
  
<223> Xaa = Unknown or Other at position 17  
  
<223> Xaa = Unknown or Other at position 60  
  
<223> Xaa = Unknown or Other at positions 62-63

<400> 245  
g aca gaa ttr att tcg tcg gct ggg gga cag tta ttc tac tcc cgc cct 49  
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro  
1 5 10 15  
  
gty gtc tca gcc aat ggc gag ccg act gtt aaa tta tat aca tct gta 97  
Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val

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	20	25	30	
gag aat gcg cag cag gac aag ggg att gcc atc cca cat gat ata gat				145
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp				
	35	40	45	
ctg ggc gac tct cgt gtg gtg atc cag gat tat gay aac car cay gaa				193
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu				
	50	55	60	
caa g				197
Gln				
65				

<210> 246  
<211> 65  
<212> PRT  
<213> Hepatitis E Virus

<220>  
<223> Xaa = Unknown or Other at position 3  
  
<223> Xaa = Unknown or Other at position 17  
  
<223> xaa = Unknown or Other at position 60  
  
<223> Xaa = Unknown or Other at positions 62-63

	20	25	30	
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro				
1	5	10	15	
Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val				
	20	25	30	
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp				
	35	40	45	
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu				
	50	55	60	
Gln				
65				

<210> 247  
<211> 418  
<212> DNA  
<213> Hepatitis E Virus

<220>  
<223> Ar1o1-f73o1pl.pat

<221> CDS  
<222> (3)...(416)

<223> Xaa = Unknown or Other at position 2  
  
<223> Xaa = Unknown or Other at position 5  
  
<223> Xaa = Unknown or Other at position 137

<400> 247

ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aac	47
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn	
1 5 10 15	
tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tcc cgt gtg	95
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val	
20 25 30	
cag acc gag att ctt att aac cta atg caa ccc cgg cag ctg gtt ttt	143
Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe	
35 40 45	
cgt cct gag gtg ctt tgg aac cat cct atc cag cgg gtt att cat aat	191
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn	
50 55 60	
gag tta gaa cag tac tgt cgg gct cgg gct ggt cgc tgc cta gag gtc	239
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val	
65 70 75	
ggg gcc cac cca agg tcc att aat gat aac cct aat gtt ttg cac cgg	287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg	
80 85 90 95	
tgc ttc cta cga cca gtc ggg agg gat gtt caa cgt tgg tat tcc gcc	335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc acc cgc ggt cct gct gcc aac tgc cgc cgt tcc gct ctg cgc ggc	383
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctc cct ccc gtc gac cgc act tac tgt yty gat gg	418
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp	
130 135	

<210> 248  
 <211> 138  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 2  
 <223> Xaa = Unknown or Other at position 5  
 <223> Xaa = Unknown or Other at position 137

<400> 248

Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser
1 5 10 15
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln
20 25 30
Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg



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      35              40              45
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
  50              55              60
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly
  65              70              75              80
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
      85              90              95
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
      100              105              110
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
      115              120              125
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
  130              135
```

<210> 249  
<211> 145  
<212> DNA  
<213> Hepatitis E Virus

<220>  
<223> Ar1-f73o2p2.pat

<221> CDS  
<222> (1)...(144)

<223> Xaa = Unknown or Other at position 1  
<223> Xaa = Unknown or Other at position 3  
<223> Xaa = Unknown or Other at position 44  
<223> Xaa = Unknown or Other at positions 46-47

```

<400> 249
gtg gtc tcr gcc aat ggc gag ccg act gtt aag cta tat aca tct gta      48
Xaa Val Xaa Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
  1              5              10              15

gag aac gcg cag cag gat aaa ggg atc gcc att cca cac gat ata gat      96
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
      20              25              30

ctg ggc gat tcc cgt gtg gtc att cag gat tat gay aac car cay gaa      144
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
      35              40              45

c                                                                    145
```

<210> 250  
<211> 48  
<212> PRT  
<213> Hepatitis E Virus

<220>  
<223> Xaa = Unknown or Other at position 1  
<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 44

<223> Xaa = Unknown or Other at positions 46-47

<400> 250

Xaa	Val	Xaa	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val
1				5					10					15	
Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Ala	Ile	Pro	His	Asp	Ile	Asp
			20					25					30		
Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Xaa	Asn	Xaa	Xaa	Glu
		35					40					45			

<210> 251

<211> 418

<212> DNA

<213> Hepatitis E Virus

<220>

<223> Ar2o1-f77o1p1.pat

<221> CDS

<222> (3)...(416)

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 41

<223> Xaa = Unknown or Other at position 44

<223> Xaa = Unknown or Other at position 93

<223> Xaa = Unknown or Other at position 137

<400> 251

ct	ggc	aty	act	act	gcy	att	gag	caa	gct	gct	ctg	gct	gcg	gct	aac	47
	Gly	Xaa	Thr	Thr	Xaa	Ile	Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	
1					5					10					15	
tct	gcc	ttg	gcg	aat	gct	gtg	gtg	gtt	cgg	ccg	ttt	cta	tcc	cgt	gtg	95
Ser	Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val	
				20					25					30		
cag	act	gag	atc	ctt	att	aac	tta	atg	car	ccc	cgg	car	ctg	gtt	ttc	143
Gln	Thr	Glu	Ile	Leu	Ile	Asn	Leu	Met	Xaa	Pro	Arg	Xaa	Leu	Val	Phe	
			35					40					45			
cgt	ccc	gag	gtg	ctt	tgg	aat	cat	ccc	att	caa	cgg	gtt	att	cat	aat	191
Arg	Pro	Glu	Val	Leu	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	
			50				55					60				
gaa	tta	gag	cag	tac	tgc	cgg	acc	cgg	gct	ggc	cgt	tgt	tta	gag	gtc	239
Glu	Leu	Glu	Gln	Tyr	Cys	Arg	Thr	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val	
			65				70					75				

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gga gcc cat cca agg tcc att aat gac aac cct aac gtt cyg cac cgg	287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Xaa His Arg	
80 85 90 95	
tgc ttc tta cga cca gtc ggg agg gat gtc caa cga tgg tac tca gcc	335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc act cgc ggc cct gcg gct aat tgc cgt cgt tcc gct ttg cgt ggt	383
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctc cct cct gtc gac cgc act tac tgt yty gat gg	418
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp	
130 135	

<210> 252  
 <211> 138  
 <212> PRT  
 <213> Hepatitis E Virus

<220>  
 <223> Xaa = Unknown or Other at position 2  
 <223> Xaa = Unknown or Other at position 5  
 <223> Xaa = Unknown or Other at position 41  
 <223> Xaa = Unknown or Other at position 44  
 <223> Xaa = Unknown or Other at position 93  
 <223> Xaa = Unknown or Other at position 137

<400> 252															
Gly	Xaa	Thr	Thr	Xaa	Ile	Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	Ser
1				5					10					15	
Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val	Gln
			20					25					30		
Thr	Glu	Ile	Leu	Ile	Asn	Leu	Met	Xaa	Pro	Arg	Xaa	Leu	Val	Phe	Arg
		35					40					45			
Pro	Glu	Val	Leu	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu
	50					55					60				
Leu	Glu	Gln	Tyr	Cys	Arg	Thr	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val	Gly
65					70					75					80
Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Xaa	His	Arg	Cys
				85					90					95	
Phe	Leu	Arg	Pro	Val	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala	Pro
			100					105					110		
Thr	Arg	Gly	Pro	Ala	Ala	Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly	Leu
		115					120					125			
Pro	Pro	Val	Asp	Arg	Thr	Tyr	Cys	Xaa	Asp						
		130				135									

<210> 253  
 <211> 197

<212> DNA  
 <213> Hepatitis E Virus

<220>  
 <223> Ar2o2-f7702.pat

<221> CDS  
 <222> (2)...(196)

<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

<400> 253  
 g aca gaa ttr att tcg tcg gct ggg ggt cag ttg ttt tac tcc cgc cct 49  
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro  
 1 5 10 15  
 gtc gtc tca gcc aat ggc gag ccg act gtt aag ttg tat aca tct gtg 97  
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val  
 20 25 30  
 gag aat gcg cag cag gat aaa gga atc gcc atc cca cac gac ata gat 145  
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp  
 35 40 45  
 ctg ggc gat tcc cgt gtg gtt att cag gat tat gay aac car cay gaa 193  
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu  
 50 55 60  
 caa g 197  
 Gln  
 65

<210> 254  
 <211> 65  
 <212> PRT  
 <213> Hepatits E Virus

<220>  
 <223> Xaa = Unknown or Other at position 3  
 <223> Xaa = Unknown or Other at position 60  
 <223> Xaa = Unknown or Other at positions 62-63

<400> 254  
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro  
 1 5 10 15  
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val  
 20 25 30  
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp  
 35 40 45  
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu

	50	55	60	
Gln				
65				
	<210> 255			
	<211> 23			
	<212> DNA			
	<213> Hepatits E Virus			
	<220>			
	<223> HEVConsORF 1N-a1			
	<400> 255			
	ccrtcrarrc artaggtgcg gtc			23
	<210> 256			
	<211> 25			
	<212> DNA			
	<213> Hepatits E Virus			
	<220>			
	<223> HEVConsORF 2N-a1			
	<400> 256			
	cytgytctrtg ytggttrtca taatc			25
	<210> 257			
	<211> 21			
	<212> DNA			
	<213> Hepatits E Virus			
	<220>			
	<223> HEVConsORF 1N-s2			
	<400> 257			
	cygccytkgc gaatgctgtg g			21
	<210> 258			
	<211> 25			
	<212> DNA			
	<213> Hepatits E Virus			
	<220>			
	<223> HEVConsORF 2N-a2			
	<400> 258			
	gytctrtgytg rttrtcataa tcctg			25